

**84569, A NOVEL HUMAN MAP KINASE FAMILY MEMBER AND USES
THEREFOR**

Cross-References to Related Applications

[0001] This application claims the benefit of U.S. Provisional Application Number 60/395,943 filed July 15, 2002, the contents of which are incorporated herein by this reference.

Background of the Invention

[0002] Obesity represents the most prevalent of body weight disorders, affecting an estimated 30 to 50% of the middle-aged population in the western world. Other body weight disorders, such as anorexia nervosa and bulimia nervosa, which together affect approximately 0.2% of the female population of the western world, also pose serious health threats. Further, such disorders as anorexia and cachexia (wasting) are also prominent features of other diseases such as cancer, cystic fibrosis, and AIDS.

[0003] Obesity, defined as a body mass index (BMI) of 30 kg/m^2 or more, contributes to diseases such as coronary artery disease, hypertension, stroke, diabetes, hyperlipidemia and some cancers. (See, *e.g.*, Nishina, P.M. *et al.* (1994), *Metab.* 43:554-558; Grundy, S. M. & Barnett, J.P. (1990), *Dis. Mon.* 36:641-731). Obesity is a complex multifactorial chronic disease that develops from an interaction of genotype and the environment and involves social, behavioral, cultural, physiological, metabolic and genetic factors.

[0004] Diabetes mellitus is the most common metabolic disease worldwide. Daily 1700 new cases of diabetes are diagnosed in the United States, while at least one-third of the 16 million Americans with diabetes are unaware of it. Diabetes is the leading cause of blindness, renal failure, and lower limb amputations in adults and is a major risk factor for cardiovascular disease and stroke. Normal glucose homeostasis requires the finely tuned orchestration of insulin secretion by pancreatic beta cells in response to subtle changes in blood glucose levels, delicately balanced with secretion of counter-regulatory hormones such as glucagon. One of the fundamental actions of insulin is to stimulate uptake of glucose from the blood into tissues, especially muscle and fat. Type 1 diabetes results from autoimmune destruction of pancreatic beta cells causing insulin deficiency. Type 2 or non-insulin-dependent diabetes mellitus (NIDDM) accounts for >90% of cases and is characterized by a triad of (1) resistance to insulin action on glucose uptake in peripheral

tissues, especially skeletal muscle and adipocytes, (2) impaired insulin action to inhibit hepatic glucose production, and (3) misregulated insulin secretion (DeFronzo, (1997) *Diabetes Rev.* 5:177-269). In most cases, type 2 diabetes is a polygenic disease with complex inheritance patterns (reviewed in Kahn *et al.*, (1996) *Annu. Rev. Med.* 47:509-531).

[0005] The identification of the role of insulin in the control of body weight was the initial identification of a hormonal signal implicated in the hormonal regulation of metabolism via the central nervous system. Subsequently, leptin, a hormone secreted by adipocytes, was identified as an additional adiposity signal. Both insulin and leptin have been shown to circulate at levels proportional to body fat content; receptors for each of these molecules have been identified in neurons in the hypothalamus, a homeostasis control center in the brain; and increases of either hormone injected into the brain result in reduced food intake while deficiency has the opposing effect (reviewed in Schwartz *et al.*, (2000) *Nature* 404:661-671). In addition to hormonal controls, neurotransmitters (e.g., serotonin and norepinephrine (NE)) as well as neuropeptides (e.g., NPY, MCH, galanin, beta-endorphin, and dynorphin) are also known to affect feeding behavior and have been implicated in regulating food intake.

[0006] Protein kinases play critical roles in the regulation of biochemical and morphological changes associated with cellular growth and division (D'Urso, G. *et al.* (1990) *Science* 250: 786-791; Birchmeier, C. *et al.* (1993) *Bioessays* 15: 185-189). They serve as growth factor receptors and signal transducers and have been implicated in diverse cellular processes (e.g., transformation and malignancy) (Hunter, T. *et al.* (1992) *Cell* 70: 375-387; Posada, J. *et al.* (1992) *Mol. Biol. Cell* 3: 583-592; Hunter, T. *et al.* (1994) *Cell* 79: 573-582). For example, protein kinases have been shown to participate in the transmission of signals from growth-factor receptors (Sturgill, T. W. *et al.* (1988) *Nature* 344: 715-718; Gomez, N. *et al.* (1991) *Nature* 353: 170-173), control of entry of cells into mitosis (Nurse, P. (1990) *Nature* 344: 503-508; Maller, J. L. (1991) *Curr. Opin. Cell Biol.* 3: 269-275) and regulation of actin bundling (Husain-Chishti, A. *et al.* (1988) *Nature* 334: 718-721). Protein kinases can be divided into two main groups based on either amino acid sequence similarity or specificity for either serine/threonine or tyrosine residues. A small number of dual-specificity kinases are structurally like the serine/threonine-specific group. Within the broad classification, kinases can be further sub-divided into families whose members share a higher degree of catalytic domain amino acid sequence identity and also have similar

biochemical properties. Most protein kinase family members also share structural features outside the kinase domain that reflect their particular cellular roles. These include regulatory domains that control kinase activity or interaction with other proteins (Hanks, S.K. et al. (1988) *Science* 241: 42-52).

[0007] Given the important biological roles and properties of kinases, there exists a need for the identification and characterization of novel kinase genes and proteins as well as for the discovery of binding agents (*e.g.*, ligands) and modulators of these nucleic acids and polypeptides for use in regulating a variety of normal and/or pathological cellular processes, including roles in metabolic disorders (*e.g.*, obesity, diabetes).

Summary of the Invention

[0008] The present invention is based, in part, on the discovery of a novel human MAP kinase family member, referred to herein as "84569". The nucleotide sequence of a cDNA encoding 84569 is shown in SEQ ID NO:1, and the amino acid sequence of an 84569 polypeptide is shown in SEQ ID NO:2. In addition, the nucleotide sequence of the coding region is depicted in SEQ ID NO:3. The 84569 nucleic acid and protein molecules of the present invention are useful as modulating agents in regulating a variety of metabolic cellular processes, *e.g.*, metabolism, satiety controls. Accordingly, in one aspect, this invention provides isolated nucleic acid molecules encoding 84569 proteins or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection of 84569-encoding nucleic acids.

[0009] In one embodiment, an 84569 nucleic acid molecule of the invention is at least 60%, 62%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more homologous to a nucleotide sequence (*e.g.*, to the entire length of the nucleotide sequence) including SEQ ID NO:1, SEQ ID NO:3, or a complement thereof.

[0010] In a preferred embodiment, the isolated nucleic acid molecule includes the nucleotide sequence shown SEQ ID NO:1 or 3, or a complement thereof. In another embodiment, the nucleic acid molecule includes SEQ ID NO:3 and nucleotides 1-296 of SEQ ID NO:1. In yet another embodiment, the nucleic acid molecule includes SEQ ID NO:3 and nucleotides 1202-4137 of SEQ ID NO:1. In another preferred embodiment, the nucleic acid molecule has the nucleotide sequence shown in SEQ ID NO:1 or 3. In another preferred embodiment, the nucleic acid molecule comprises a fragment of at least 509

nucleotides of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or a complement thereof.

[0011] In another embodiment, an 84569 nucleic acid molecule includes a nucleotide sequence encoding a protein having an amino acid sequence sufficiently homologous to the amino acid sequence of SEQ ID NO:2. In a preferred embodiment, an 84569 nucleic acid molecule includes a nucleotide sequence encoding a protein having an amino acid sequence at least 60%, 65%, 70%, 75%, 80%, 81%, 85%, 90%, 95%, 98% or more homologous to an amino acid sequence including SEQ ID NO:2 (e.g., the entire amino acid sequence of SEQ ID NO:2).

[0012] In another preferred embodiment, an isolated nucleic acid molecule encodes the amino acid sequence of a human 84569. In yet another preferred embodiment, the nucleic acid molecule includes a nucleotide sequence encoding a protein which includes the amino acid sequence of SEQ ID NO: 2. In yet another preferred embodiment, the nucleic acid molecule includes a nucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO: 2.

[0013] Another embodiment of the invention features nucleic acid molecules, preferably 84569 nucleic acid molecules, which specifically detect 84569 nucleic acid molecules relative to nucleic acid molecules encoding non-84569 proteins. For example, in one embodiment, such a nucleic acid molecule is at least 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, or 800 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1, or a complement thereof.

[0014] In other preferred embodiments, the nucleic acid molecule encodes a naturally occurring allelic variant of a polypeptide which includes the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule which includes SEQ ID NO:1 or SEQ ID NO:3 under stringent conditions.

[0015] Another embodiment of the invention provides an isolated nucleic acid molecule which is antisense to an 84569 nucleic acid molecule, e.g., the coding strand of an 84569 nucleic acid molecule.

[0016] Another aspect of the invention provides a vector comprising an 84569 nucleic acid molecule. In certain embodiments, the vector is a recombinant expression vector. In another embodiment, the invention provides a host cell containing a vector of the invention. The invention also provides a method for producing a protein, preferably an 84569 protein,

by culturing in a suitable medium, a host cell, e.g., a mammalian host cell such as a non-human mammalian cell, of the invention containing a recombinant expression vector, such that the protein is produced.

[0017] Another aspect of this invention features isolated or recombinant 84569 proteins and polypeptides. In one embodiment, the isolated protein, preferably an 84569 protein, includes at least one protein kinase domain, and at least one ATP-binding site. In another embodiment, the isolated protein, preferably an 84569 protein, includes at least one protein kinase domain, and at least one ATP-binding site and has an amino acid sequence which is at least 60%, 65%, 70%, 75%, 80%, 81%, 85%, 90%, 95%, 99% or more homologous to an amino acid sequence including SEQ ID NO:2. In yet another embodiment, the isolated protein, preferably an 84569 protein, includes at least one protein kinase domain, and at least one ATP-binding site and is expressed and/or functions in cells of the metabolic system (e.g., hypothalamic neurons). In an even further embodiment, the isolated protein, preferably an 84569 protein, includes at least one protein kinase domain, and at least one ATP-binding site and plays a role in signalling pathways associated with cellular growth, e.g., signalling pathways associated with cell cycle regulation. In another embodiment, the isolated protein, preferably an 84569 protein, includes at least one protein kinase domain, and at least one ATP-binding site and is encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3.

[0018] In another embodiment, the isolated protein, preferably an 84569 protein, has an amino acid sequence sufficiently homologous to the amino acid sequence of SEQ ID NO:2. In a preferred embodiment, the protein, preferably an 84569 protein, has an amino acid sequence at least about 60%, 65%, 70%, 75%, 80%, 81%, 85%, 90%, 95%, 98% or more homologous to an amino acid sequence including SEQ ID NO:2 (e.g., the entire amino acid sequence of SEQ ID NO:2). In another embodiment, the invention features fragments of the proteins having the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 amino acids (e.g., contiguous amino acids) of the amino acid sequence of SEQ ID NO:2. In another embodiment, the protein, preferably an 84569 protein, has the amino acid sequence of SEQ ID NO:2.

[0019] Another embodiment of the invention features an isolated protein, preferably an 84569 protein, which is encoded by a nucleic acid molecule having a nucleotide sequence at least about 60%, 65%, 70%, 75%, 78%, 80%, 85%, 86%, 90%, 95%, 97%, 98%

or more homologous to a nucleotide sequence (e.g., to the entire length of the nucleotide sequence) including SEQ ID NO:1, SEQ ID NO:3, or a complement thereof. This invention further features an isolated protein, preferably an 84569 protein, which is encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or a complement thereof.

[0020] The proteins of the present invention or biologically active portions thereof, can be operatively linked to a non-84569 polypeptide (e.g., heterologous amino acid sequences) to form fusion proteins. The invention further features antibodies, such as monoclonal or polyclonal antibodies, that specifically bind proteins of the invention, preferably 84569 proteins. In addition, the 84569 proteins or biologically active portions thereof can be incorporated into pharmaceutical compositions, which optionally include pharmaceutically acceptable carriers.

[0021] The present invention is based, at least in part, on the discovery that 84569 molecules are expressed at increased levels in hypothalamic tissue, e.g., arcuate nucleus, ventromedial nucleus (see Examples 1-3 and Tables 1-5 described herein). 84569 molecules were further found to be upregulated in ob/ob and Agouti mice (i.e., under genetic conditions that affect metabolism, e.g., obesity) (see Example 3 and Table 5). Furthermore, overexpression of 84569 in neural cells can negatively affect leptin receptor signaling.

[0022] Accordingly, the present invention provides methods for the diagnosis and treatment of metabolic disorders including but not limited to obesity, anorexia, cachexia, and diabetes.

[0023] In one aspect, the invention provides methods of screening for compounds that modulate the expression or activity of the 84569 polypeptides or nucleic acids. The method includes contacting a sample expressing an 84569 nucleic acid or polypeptide with a test compound and assaying the ability of the test compound to modulate the expression of an 84569 nucleic acid or the activity of an 84569 polypeptide.

[0024] In one embodiment, the invention provides methods for identifying a compound capable of treating a metabolic disorder, e.g., obesity, anorexia, cachexia, and diabetes. The method includes assaying the ability of the compound to modulate 84569 nucleic acid expression or 84569 polypeptide activity.

[0025] In still another aspect, the invention provides a process for modulating 84569 polypeptide or nucleic acid expression or activity, e.g. using the screened compounds. In

certain embodiments, the methods involve treatment of conditions related to aberrant activity or expression of the 84569 polypeptides or nucleic acids, such as conditions involving aberrant or deficient cellular signaling, proliferation or differentiation.

[0026] The invention also provides assays for determining the activity of or the presence or absence of 84569 polypeptides or nucleic acid molecules in a biological sample, including for metabolic disease diagnosis (e.g., obesity). In one aspect, provided are assays for determining the presence or absence of a genetic alteration in an 84569 polypeptide or nucleic acid molecule, including for disease diagnosis.

[0027] In one embodiment, methods include identifying a nucleic acid associated with a metabolic disorder, e.g., obesity, anorexia, cachexia, and diabetes.

[0028] In yet another aspect, the invention features a method for identifying a subject having a metabolic disorder characterized by aberrant 84569 polypeptide activity or aberrant 84569 nucleic acid expression, e.g., obesity, anorexia, or cachexia. The method includes contacting a sample obtained from the subject and expressing an 84569 nucleic acid or polypeptide with a test compound and assaying the ability of the test compound to modulate the expression of an 84569 nucleic acid or the activity of an 84569 polypeptide.

[0029] In yet another aspect, the invention features a method for treating a subject having a metabolic disorder characterized by aberrant 84569 polypeptide activity or aberrant 84569 nucleic acid expression, e.g., obesity, diabetes, or cachexia. The method includes administering to the subject an 84569 modulator, e.g., in a pharmaceutically acceptable formulation or by using a gene therapy vector. Embodiments of this aspect of the invention include the 84569 modulator being any of a small molecule, an anti-84569 antibody, an 84569 polypeptide comprising the amino acid sequence of SEQ ID NO:2 or a fragment thereof, an 84569 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, an antisense 84569 nucleic acid molecule, a nucleic acid molecule of SEQ ID NO:1 or a fragment thereof, or a ribozyme.

[0030] Other features and advantages of the invention will be apparent from the following detailed description and claims.

Detailed Description of the Invention

[0031] Here we describe a novel MAP kinase, 84569, which is highly and specifically expressed in human and mouse hypothalamus and which expression is regulated under genetic conditions that result in obesity. 84569 is therefore a candidate target to identify small molecules for the treatment of metabolic disorders, including diabetes, obesity, cachexia, and/or feeding disorders in humans.

Human 84569

[0032] The human 84569 sequence (SEQ ID NO:1), which is approximately 2230 nucleotides long including untranslated regions, contains a predicted methionine-initiated coding sequence of about 2208 nucleotides (nucleotides 1-2208 of SEQ ID NO:1; SEQ ID NO:3), not including the terminal codon. The coding sequence encodes a 735 amino acid protein (SEQ ID NO:2).

[0033] The 84569 protein includes the following domains: one, two, three, four, five, six, seven, preferably eight N-glycosylation site (PS00001) located at about amino acids 61-64, 289-292, 312-315, 341-344, 392-395, 400-403, 624-627, 647-650 of SEQ ID NO:2; one glycosaminoglycan attachment site at about amino acids 649-652 of SEQ ID NO:2; one, two, preferably three cAMP- and cGMP-dependent protein kinase phosphorylation site (PS00004) located at about amino acids 6-9, 17-20, 102-105 of SEQ ID NO:2; one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, preferably nineteen predicted protein kinase C phosphorylation sites (PS00005) located at about amino acids 10-12, 13-15, 30-32, 84-86, 100-102, 105-107, 113-115, 124-126, 152-154, 185-187, 202-204, 240-242, 267-269, 271-273, 417-419, 425-427, 459-461, 503-505, and 669-671 of SEQ ID NO:2; one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, preferably sixteen predicted casein kinase II phosphorylation sites (PS00006) located at about amino acids 84-87, 111-114, 170-173, 179-182, 185-188, 215-218, 221-224, 225-228, 240-243, 302-305, 402-405, 417-420, 469-472, 626-629, 663-666, and 729-732 of SEQ ID NO:2; one predicted tyrosine kinase phosphorylation site (PS00007) located at about amino acids 505-512 of SEQ ID NO:2; one, two, three, four, five, six, preferably seven predicted N-myristoylation sites (PS00008) located at about amino acids 29-34, 378-383, 477-482, 490-495, 552-557, 622-627, and 687-692 of SEQ ID NO:2; one, preferably two predicted amidation site (PS00009) located at about amino acids 100-103, 651-654 of SEQ ID NO:2; one predicted protein

kinase ATP-binding region signature site (PS00107) located at about amino acids 474-496 of SEQ ID NO:2; one predicted serine/threonine kinase active site signature site (PS00108) located at about amino acids 589-601 of SEQ ID NO:2; and one aminoacyl-transfer RNA synthetase class II signature 2 site (PS00339) located at about amino acids 674-683 of SEQ ID NO:2.

[0034] Based on 84569 protein sequence, cellular localization signals can be identified by methods known to one of skill in the art (e.g., PSORT Prediction). Predicted subcellular localization of 84569, generated using PSORT Prediction software is that it is nuclear.

[0035] For general information regarding PSORT, Prosite and PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997) *Protein* 28:405-420 and <http://www.psc.edu/general/software/packages/pfam/pfam.html>.

[0036] The 84569 protein contains a significant number of structural characteristics in common with members of the MAP kinase family. The term "family" when referring to the protein and nucleic acid molecules of the invention means two or more proteins or nucleic acid molecules having a common structural domain or motif and having sufficient amino acid or nucleotide sequence homology as defined herein. Such family members can be naturally or non-naturally occurring and can be from either the same or different species. For example, a family can contain a first protein of human origin as well as other distinct proteins of human origin, or alternatively, can contain homologues of non-human origin, e.g., rat or mouse proteins. Members of a family can also have common functional characteristics.

[0037] In one embodiment, the isolated proteins of the present invention, preferably 84569 proteins, are identified based on the presence of at least one "protein kinase domain" and at least one "ATP-binding region." As used herein, the term "protein kinase domain" includes an amino acid sequence of about 200-400 amino acid residues in length, preferably 200-300 amino acid residues in length, and more preferably 250-275 amino acid residues in length, which is conserved in kinases which phosphorylate serine and threonine residues and found in the catalytic domain of Ser/Thr kinases. The protein kinase domain of 84569 is aligned with the PFAM consensus protein kinase domain (SEQ ID NO:4) in Table 1 (invariant residues are indicated by upper case letters and nearly invariant residues are indicated by lower case letters). The nearly invariant residues are usually found in most Ser/Thr kinase sites, but can be replaced by other amino acids which, preferably, have similar characteristics. For example, a nearly invariant hydrophobic amino acid in the above

amino acid consensus sequence would most likely be replaced by another hydrophobic amino acid. Protein kinase domains, including Ser/Thr kinase domains are described in, for example, Levin D.E. et al. (1990) Proc. Natl. Acad. Sci. USA 87:8272-76, the contents of which are incorporated herein by reference.

Table 1. Alignment of 84569 and PFAM consensus Protein Kinase Domain

pkinase: domain 1 of 1, from 468 to 731: score 296.0, E = 4.7e-85

Kinase domain homology: 33 % identical: 74% similarity

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      *->yelleklGeGsfgkVykakhkdktgkiVAvKilkk.....ekes
      ++++e+lG+G++G+Vy +      g++ AvK++ ++++++ eke+
84569  468  WTKGEILGKGAYGTVYCGLTS--QGQLIAVKQVALdtsnklaaEKEY 512

      ikekrflrEiqilkrLsHpNivrligvfedtdhlylvmEymegGdLfdy
      k  ++ E+ +lk L+H Niv ++g++  ++ + + mE+++gG+  ++
84569  513  RK---LQEEVDLLKALKHVNIVAYLGTCCL-QENTVSIFMEFVPGGSISSI 558

      lrrnggplsekeakkialQilrGleYlHsngivHRDLKpeNILldendgt
      + r g pl+e  +k+++Qil+G++YLH+n +vHRD+K  N++l  g
84569  559  INRFG-PLPEMVFCYTKQILQGVAYLHENCVVHRDIKGNVMLMPT-GI 606

      vKiaDFGLArlle.....ssskltttfvGTpwYmmAPEvilegrgyssk
      +K++DFG Ar l  ++ ++++s +l++  Gtp++m APEv  ++ +gy++k
84569  607  IKLIDFGCARRLAwtglngtHSDMLKSMHGTPYWM-APEV-INESGYGRK 654

      vDvWSlGviLyElltggpplfpgadlpaftggdevdqliifvklPfsdel
      +D+WS+G++++E++tg                                k+P
84569  655  SDIWSIGCTVFEMATG-----KPPLAS-- 676

      pktridpleelfriikrpglrlplpsncSeelkdLlkkcLnkDPskRpGs
      +d ++++f+i  ++gl +plp+++Se++ d+++ cL++D ++Rp
84569  677  ----MDRMAAMFYIGAHRGLMPPLPDHFSENAADFVRMCLTRDQHERP-- 720

      atakeilnhpwf<-*
      +a ++l+h ++
84569  721  -SALQLLKHSFL      731

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[0038] As used herein, the term "ATP-binding region" includes an amino acid sequence of about 20-40, preferably 20-30, and more preferably 20-25 amino acid residues in length, present in enzymes which activate their substrates by phosphorylation, and involved in binding adenosine triphosphate (ATP). ATP-binding regions preferably include the following amino acid consensus sequence: G-X-G-X-X-G-X(15-23)-K(SEQ ID NO:5).

ATP-binding regions are described in, for example, Samuel K.P. et al. (1987) FEBS Let. 218(1): 81-86, the contents of which are incorporated herein by reference. Amino acid residues 474-496 of 84569 comprise an ATP-binding region.

[0039] Isolated proteins of the present invention, preferably 84569 proteins, have an amino acid sequence sufficiently homologous to the amino acid sequence of SEQ ID NO:2 or are encoded by a nucleotide sequence sufficiently homologous to SEQ ID NO:1 or SEQ ID NO:3. As used herein, the term "sufficiently homologous" refers to a first amino acid or nucleotide sequence which contains a sufficient or minimum number of identical or equivalent (e.g., an amino acid residue which has a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences share common structural domains or motifs and/or a common functional activity. For example, amino acid or nucleotide sequences which share common structural domains have at least 30%, 40%, or 50% homology, preferably 60% homology, more preferably 70%-80%, and even more preferably 90-95% homology across the amino acid sequences of the domains and contain at least one and preferably two structural domains or motifs, are defined herein as sufficiently homologous. Furthermore, amino acid or nucleotide sequences which share at least 30%, 40%, or 50%, preferably 60%, more preferably 70-80%, or 90-95% homology and share a common functional activity are defined herein as sufficiently homologous.

[0040] As used interchangeably herein a "84569 activity", "biological activity of 84569" or "functional activity of 84569", refers to an activity exerted by an 84569 protein, polypeptide or nucleic acid molecule on an 84569 responsive cell or an 84569 protein substrate, as determined in vivo, or in vitro, according to standard techniques. The biological activity of 84569 is described herein.

[0041] Accordingly, another embodiment of the invention features isolated 84569 proteins and polypeptides having an 84569 activity. Preferred proteins are 84569 proteins having at least one protein kinase site and at least one ATP-binding region and, preferably, an 84569 activity. Additional preferred proteins have at least one protein kinase site and at least one ATP-binding region and are, preferably, encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3.

[0042] The nucleotide sequence of the isolated human 84569 cDNA and the predicted amino acid sequence of the human 84569 polypeptide are shown in SEQ ID NOs:1 and 2, respectively. A plasmid containing the nucleotide sequence encoding human 84569 was deposited with American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209, on _____ and assigned Accession Number _____. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. §112.

[0043] The 84569 gene, which is approximately 2208 nucleotides in length, encodes a protein which is approximately 735 amino acid residues in length. The 84569 gene is expressed predominantly in brain, particularly the hypothalamus.

[0044] As the 84569 polypeptides of the invention may modulate 84569-mediated activities, they may be useful for developing novel diagnostic and therapeutic agents for 84569-mediated or related disorders, as described below.

[0045] As used herein, the term "protein kinase" includes a protein or polypeptide which is capable of modulating its own phosphorylation state or the phosphorylation state of another protein or polypeptide. Protein kinases can have a specificity for (i.e., a specificity to phosphorylate) serine/threonine residues, tyrosine residues, or both serine/threonine and tyrosine residues, e.g., the dual specificity kinases. As referred to herein, protein kinases preferably include a catalytic domain of about 200-400 amino acid residues in length, preferably about 200-300 amino acid residues in length, or more preferably about 250-300 amino acid residues in length, which includes preferably 5-20, more preferably 5-15, or preferably 11 highly conserved motifs or subdomains separated by sequences of amino acids with reduced or minimal conservation. Specificity of a protein kinase for phosphorylation of either tyrosine or serine/threonine can be predicted by the sequence of two of the subdomains (VIb and VIII) in which different residues are conserved in each class (as described in, for example, Hanks et al. (1988) Science 241:42-52) the contents of which are incorporated herein by reference). These subdomains are also described in further detail herein.

[0046] Protein kinases play a role in signalling pathways associated with cellular growth and functioning. For example, protein kinases are involved in the regulation of signal transmission from cellular receptors, e.g., growth-factor receptors; entry of cells into

mitosis; and the regulation of cytoskeleton function, e.g., actin bundling. Thus, the 84569 molecules of the present invention may be involved in: 1) the regulation of transmission of signals from cellular receptors, e.g., metabolic receptors; 2) the modulation of the entry of cells, e.g., metabolic precursor cells, into mitosis; 3) the modulation of cellular differentiation; 4) the modulation of cell death; and 5) the regulation of cytoskeleton function, e.g., actin bundling.

[0047] As used herein, the term “metabolic disorder” includes a disorder, disease or condition which is caused or characterized by an abnormal metabolism (i.e., the chemical changes in living cells by which energy is provided for vital processes and activities) in a subject. Metabolic disorders include diseases, disorders, or conditions associated with aberrant feeding activity or aberrant neuronal (e.g., hypothalamic neuronal cell) signaling or function. Metabolic disorders can be characterized by a misregulation (e.g., downregulation or upregulation) of 84569 activity. Metabolic disorders can detrimentally affect cellular functions such as cellular proliferation, growth, differentiation, or migration, cellular regulation of homeostasis, inter- or intra-cellular communication; tissue function, such as liver function, muscle function, or adipocyte function; systemic responses in an organism, such as hormonal responses (e.g., insulin and/or leptin response) or satiety responses. Examples of metabolic disorders include obesity, diabetes, hyperphagia, endocrine abnormalities, triglyceride storage disease, Bardet-Biedl syndrome, Lawrence-Moon syndrome, Prader-Labhart-Willi syndrome, hypophagia, anorexia, and cachexia. Obesity is defined as a body mass index (BMI) of $30 \text{ kg}^2/\text{m}^2$ or more (National Institute of Health, Clinical Guidelines on the Identification, Evaluation, and Treatment of Overweight and Obesity in Adults (1998)). However, the present invention is also intended to include a disease, disorder, or condition that is characterized by a body mass index (BMI) of $25 \text{ kg}^2/\text{m}^2$ or more, $26 \text{ kg}^2/\text{m}^2$ or more, $27 \text{ kg}^2/\text{m}^2$ or more, $28 \text{ kg}^2/\text{m}^2$ or more, $29 \text{ kg}^2/\text{m}^2$ or more, $29.5 \text{ kg}^2/\text{m}^2$ or more, or $29.9 \text{ kg}^2/\text{m}^2$ or more, all of which are typically referred to as overweight (National Institute of Health, Clinical Guidelines on the Identification, Evaluation, and Treatment of Overweight and Obesity in Adults (1998)).

[0048] As used interchangeably herein, “84569 activity,” “biological activity of 84569” or “functional activity of 84569,” includes an activity exerted by an 84569 protein, polypeptide or nucleic acid molecule on an 84569 responsive cell or tissue, e.g., hypothalamic neurons, or on an 84569 protein ligand, as determined in vivo, or in vitro, according to standard techniques. 84569 activity can be a direct activity, such as an

association with an 84569-target molecule. As used herein, a "ligand" or "substrate" or "target molecule" or "binding partner" is a molecule with which an 84569 protein binds or interacts in nature, such that 84569-mediated function, e.g., modulation of metabolism, is achieved. An 84569 target molecule can be a non-84569 molecule or an 84569 protein or polypeptide. Examples of such target molecules include proteins in the same signaling path as the 84569 protein, e.g., proteins which may function upstream (including both stimulators and inhibitors of activity) or downstream of the 84569 protein in a pathway involving regulation of metabolism, e.g., an 84569 ligand. 84569 target molecules may include for example small molecules, such as phosphate ions, which binds kinases such as 84569. Alternatively, an 84569 activity is an indirect activity, such as a cellular signaling activity mediated by interaction of the 84569 protein with an 84569 target molecule. The biological activities of 84569 are described herein. For example, the 84569 proteins can have one or more of the following activities: 1) modulation of fat homeostasis; 2) modulation of satiety controls (e.g., signals necessary for metabolic regulation); 3) modulation of lipolysis (e.g., fat mobilization necessary as an energy source and/or for thermogenesis); 4) modulation of energy expenditure 5) modulation of feeding behavior 6) modulation of signaling for maintenance of energy homeostasis, 7) interaction with (e.g., bind to) phosphate; 8) interaction with (e.g., bind to) an 84569 ligand protein which naturally binds to 84569; 9) modulation of hypothalamic neuron signaling; 10) modulation of the activity of leptin signaling (e.g., a leptin receptor signaling pathway); 11) modulation of a cytosolic ion, e.g., calcium, concentration; 12) modulation of the release of a neurotransmitter, e.g., acetylcholine, from a neuron, e.g., a presynaptic neuron; 13) signaling of ligand binding via phosphatidylinositol turnover; and 14) modulation of, e.g., activation or inhibition, phospholipase C activity.

[0049] As used herein, "metabolic activity" may include an activity exerted by a cell, e.g., a neuronal cell such as for example a hypothalamic neuronal cell, or an activity that takes place in a neuronal cell. For example, such activities include cellular processes that contribute to the physiological role of hypothalamic neuronal cells (whether directly or indirectly, e.g., through signaling), in regulation of metabolism and satiety controls and include, but are not limited to, cell proliferation, differentiation, growth, migration, programmed cell death, uncoupled mitochondrial respiration, thermogenesis, and transmission of neurotransmitters.

[0050] The 84569 protein, fragments thereof, and derivatives and other variants of the sequence in SEQ ID NO:2 are collectively referred to as "polypeptides or proteins of the invention" or "84569 polypeptides or proteins". Nucleic acid molecules encoding such polypeptides or proteins are collectively referred to as "nucleic acids of the invention" or "84569 nucleic acids." 84569 molecules refer to 84569 nucleic acids, polypeptides, and antibodies.

[0051] As used herein, the term "nucleic acid molecule" includes DNA molecules (e.g., a cDNA or genomic DNA) and RNA molecules (e.g., an mRNA) and analogs of the DNA or RNA generated, e.g., by the use of nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

[0052] The term "isolated or purified nucleic acid molecule" includes nucleic acid molecules which are separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. For example, with regards to genomic DNA, the term "isolated" includes nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and/or 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of 5' and/or 3' nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

[0053] As used herein, the term "hybridizes under stringent conditions" describes conditions for hybridization and washing. Stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Aqueous and nonaqueous methods are described in that reference and either can be used. A preferred, example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50°C. Another example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 55°C. A further example of

stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 60°C. Preferably, stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C. Particularly preferred stringency conditions (and the conditions that should be used if the practitioner is uncertain about what conditions should be applied to determine if a molecule is within a hybridization limitation of the invention) are 0.5M Sodium Phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1, or SEQ ID NO:3, corresponds to a naturally-occurring nucleic acid molecule.

[0054] As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

[0055] As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules which include an open reading frame encoding an 84569 protein, preferably a mammalian 84569 protein, and can further include non-coding regulatory sequences, and introns.

[0056] An "isolated" or "purified" polypeptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. In one embodiment, the language "substantially free" means preparation of 84569 protein having less than about 30%, 20%, 10% and more preferably 5% (by dry weight), of non-84569 protein (also referred to herein as a "contaminating protein"), or of chemical precursors or non-84569 chemicals. When the 84569 protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The invention includes isolated or purified preparations of at least 0.01, 0.1, 1.0, and 10 milligrams in dry weight.

[0057] A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of 84569(e.g., the sequence of SEQ ID NO:1 or SEQ ID NO:3, without abolishing or more preferably, without substantially altering a biological activity, whereas

an "essential" amino acid residue results in such a change. For example, amino acid residues that are conserved among the polypeptides of the present invention, e.g., those present in the catalytic protein kinase domain, are predicted to be particularly unamenable to alteration.

[0058] A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an 84569 protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an 84569 coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for 84569 biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:1 or SEQ ID NO:3, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

[0059] As used herein, a "biologically active portion" of an 84569 protein includes a fragment of an 84569 protein which participates in an interaction between an 84569 molecule and a non-84569 molecule. Biologically active portions of an 84569 protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the 84569 protein, e.g., the amino acid sequence shown in SEQ ID NO:2, which include less amino acids than the full length 84569 proteins, and exhibit at least one activity of an 84569 protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the 84569 protein, e.g., protein kinase activity. A biologically active portion of an 84569 protein can be a polypeptide which is, for example, 10, 25, 50, 100, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more amino acids in length. Biologically active portions of an 84569 protein can be used as targets for developing agents which modulate an 84569 mediated activity, e.g., protein kinase activity.

[0060] Calculations of homology or sequence identity between sequences (the terms are used interchangeably herein) are performed as follows.

[0061] To determine the percent identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, 90%, 100% of the length of the reference sequence (e.g., when aligning a second sequence to the 84569 amino acid sequence of SEQ ID NO:2 having 735 amino acid residues, at least 305, preferably at least 378, more preferably at least 452, even more preferably at least 208, and even more preferably at least 525, 598, 672, or 735 amino acid residues are aligned. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

[0062] The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to

determine if a molecule is within a sequence identity or homology limitation of the invention) is using a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

[0063] The percent identity between two amino acid or nucleotide sequences can be determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

[0064] The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al., (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 84569 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 84569 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

[0065] "Misexpression or aberrant expression", as used herein, refers to a non-wild type pattern of gene expression, at the RNA or protein level. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

[0066] "Subject", as used herein, can refer to a mammal, e.g., a human, or to an experimental or animal or disease model. The subject can also be a non-human animal, e.g., a horse, cow, goat, or other domestic animal.

[0067] A "purified preparation of cells", as used herein, refers to, in the case of plant or animal cells, an in vitro preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

[0068] The present invention is based, at least in part, on the discovery that 84569 molecules are expressed at increased levels in hypothalamic tissue, e.g., arcuate nucleus, ventromedial nucleus (see Examples 1-3 and Tables 1-5 described herein). 84569 molecules were further found to be upregulated in ob/ob and Agouti mice (i.e., under genetic conditions that affect metabolism, e.g., obesity) (see Example 3 and Table 6). Furthermore, overexpression of 84569 in neural cells can negatively affect leptin receptor signaling. Thus, the compositions and methods described herein are useful in the diagnosis and treatment of metabolic disorders.

[0069] Various aspects of the invention are described in further detail below.

Isolated Nucleic Acid Molecules

[0070] In one aspect, the invention provides, an isolated or purified, nucleic acid molecule that encodes an 84569 polypeptide described herein, e.g., a full length 84569 protein or a fragment thereof, e.g., a biologically active portion of 84569 protein. Also included is a nucleic acid fragment suitable for use as a hybridization probe, which can be used, e.g., to identify nucleic acid molecule encoding a polypeptide of the invention, 84569 mRNA, and fragments suitable for use as primers, e.g., PCR primers for the amplification or mutation of nucleic acid molecules.

[0071] In one embodiment, an isolated nucleic acid molecule of the invention includes the nucleotide sequence shown in SEQ ID NO:1, or a portion of any of these nucleotide sequences. In one embodiment, the nucleic acid molecule includes sequences encoding the human 84569 protein (i.e., "the coding region", from nucleotides 1-2208 of SEQ ID NO:1, not including the terminal codon), as well as 3' untranslated sequences (nucleotides 2209-2230 of SEQ ID NO:1). Alternatively, the nucleic acid molecule can include only the coding region of SEQ ID NO:1 (e.g., nucleotides 1-2208 of SEQ ID NO:1, corresponding to

SEQ ID NO:3) and, e.g., no flanking sequences which normally accompany the subject sequence.

[0072] In another embodiment, an isolated nucleic acid molecule of the invention includes a nucleic acid molecule which is a complement of the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, or a portion of any of these nucleotide sequences. In other embodiments, the nucleic acid molecule of the invention is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3, such that it can hybridize to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3, thereby forming a stable duplex.

[0073] In one embodiment, an isolated nucleic acid molecule of the present invention includes a nucleotide sequence which is at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more homologous to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3. In the case of an isolated nucleic acid molecule which is longer than or equivalent in length to the reference sequence, e.g., SEQ ID NO:1, or SEQ ID NO:3, the comparison is made with the full length of the reference sequence. Where the isolated nucleic acid molecule is shorter than the reference sequence, e.g., shorter than SEQ ID NO:1, or SEQ ID NO:3, the comparison is made to a segment of the reference sequence of the same length (excluding any loop required by the homology calculation).

84569 Nucleic Acid Fragments

[0074] A nucleic acid molecule of the invention can include only a portion of the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:3. For example, such a nucleic acid molecule can include a fragment which can be used as a probe or primer or a fragment encoding a portion of an 84569 protein, e.g., an immunogenic or biologically active portion of an 84569 protein. A fragment can comprise: nucleotides 1404-2193 of SEQ ID NO:1, which encodes an protein kinase domain of human 84569. The nucleotide sequence determined from the cloning of the 84569 gene allows for the generation of probes and primers designed for use in identifying and/or cloning other 84569 family members, or fragments thereof, as well as 84569 homologues, or fragments thereof, from other species.

[0075] In another embodiment, a nucleic acid includes a nucleotide sequence that includes part, or all, of the coding region and extends into either (or both) the 5' or 3' noncoding region. Other embodiments include a fragment which includes a nucleotide sequence encoding an

amino acid fragment described herein. Nucleic acid fragments can encode a specific domain or site described herein or fragments thereof, particularly fragments thereof which are at least 150 amino acids in length. Fragments also include nucleic acid sequences corresponding to specific amino acid sequences described above or fragments thereof. Nucleic acid fragments should not be construed as encompassing those fragments that may have been disclosed prior to the invention.

[0076] A nucleic acid fragment can include a sequence corresponding to a domain, region, or functional site described herein. A nucleic acid fragment can also include one or more domain, region, or functional site described herein. Thus, for example, the nucleic acid fragment can include an protein kinase domain. In a preferred embodiment the fragment is at least, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, or 2200 base pairs in length.

[0077] 84569 probes and primers are provided. Typically a probe/primer is an isolated or purified oligonucleotide. The oligonucleotide typically includes a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, 12 or 15, preferably about 20 or 25, more preferably about 30, 35, 40, 45, 50, 55, 60, 65, or 75 consecutive nucleotides of a sense or antisense sequence of SEQ ID NO:1, SEQ ID NO:3, or of a naturally occurring allelic variant or mutant of SEQ ID NO:1 or SEQ ID NO:3.

[0078] In a preferred embodiment the nucleic acid is a probe which is at least 5 or 10, and less than 200, more preferably less than 100, or less than 50, base pairs in length. It should be identical, or differ by 1, or less than in 5 or 10 bases, from a sequence disclosed herein. If alignment is needed for this comparison the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

[0079] A probe or primer can be derived from the sense or anti-sense strand of a nucleic acid which encodes an protein kinase domain (e.g., about amino acid residues 468-731 of SEQ ID NO:2).

[0080] In another embodiment a set of primers is provided, e.g., primers suitable for use in a PCR, which can be used to amplify a selected region of an 84569 sequence, e.g., a region described herein. The primers should be at least 5, 10, or 50 base pairs in length and less than 100, or less than 200, base pairs in length. The primers should be identical, or differs by one base from a sequence disclosed herein or from a naturally occurring variant. E.g., primers suitable for amplifying all or a portion of any of the following regions are

provided: an protein kinase domain (e.g., about amino acid residues 468-731 of SEQ ID NO:2).

[0081] A nucleic acid fragment can encode an epitope bearing region of a polypeptide described herein.

[0082] A nucleic acid fragment encoding a "biologically active portion of an 84569 polypeptide" can be prepared by isolating a portion of the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3, which encodes a polypeptide having an 84569 biological activity (e.g., the biological activities of the 84569 proteins as described herein), expressing the encoded portion of the 84569 protein (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the 84569 protein. For example, a nucleic acid fragment encoding a biologically active portion of 84569 includes an protein kinase domain (e.g., about amino acid residues 468-731 of SEQ ID NO:2). A nucleic acid fragment encoding a biologically active portion of an 84569 polypeptide, may comprise a nucleotide sequence which is greater than 300-1200 or more nucleotides in length.

[0083] In preferred embodiments, nucleic acids include a nucleotide sequence which is about 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200 nucleotides in length and hybridizes under stringent hybridization conditions to a nucleic acid molecule of SEQ ID NO:1, or SEQ ID NO:3.

84569 Nucleic Acid Variants

[0084] The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3. Such differences can be due to degeneracy of the genetic code (and result in a nucleic acid which encodes the same 84569 proteins as those encoded by the nucleotide sequence disclosed herein. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence which differs, by at least 1, but less than 5, 10, 20, 50, or 100 amino acid residues that shown in SEQ ID NO:2. If alignment is needed for this comparison the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

[0085] Nucleic acids of the inventor can be chosen for having codons, which are preferred, or non preferred, for a particular expression system. E.g., the nucleic acid can be one in which at least one codon, at preferably at least 10%, or 20% of the codons has been

altered such that the sequence is optimized for expression in E. coli, yeast, human, insect, or CHO cells.

[0086] Nucleic acid variants can be naturally occurring, such as allelic variants (same locus), homologs (different locus), and orthologs (different organism) or can be non-naturally occurring. Non-naturally occurring variants can be made by mutagenesis techniques, including those applied to polynucleotides, cells, or organisms. The variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product).

[0087] In a preferred embodiment, the nucleic acid differs from that of SEQ ID NO:1 or SEQ ID NO:3, e.g., as follows: by at least one but less than 10, 20, 30, or 40 nucleotides; at least one but less than 1%, 5%, 10% or 20% of the in the subject nucleic acid. If necessary for this analysis the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

[0088] Orthologs, homologs, and allelic variants can be identified using methods known in the art. These variants comprise a nucleotide sequence encoding a polypeptide that is 50%, at least about 55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more identical to the amino acid sequence shown in SEQ ID NO:2 or a fragment of this sequence. Such nucleic acid molecules can readily be obtained as being able to hybridize under stringent conditions, to the nucleotide sequence shown in SEQ ID NO:3 or a fragment of this sequence. Nucleic acid molecules corresponding to orthologs, homologs, and allelic variants of the 84569 cDNAs of the invention can further be isolated by mapping to the same chromosome or locus as the 84569 gene. Preferred variants include those that are correlated with protein kinase activity.

[0089] Allelic variants of 84569, e.g., human 84569, include both functional and non-functional proteins. Functional allelic variants are naturally occurring amino acid sequence variants of the 84569 protein within a population that maintain the ability to modulate the phosphorylation state of itself or another protein or polypeptide. Functional allelic variants will typically contain only conservative substitution of one or more amino acids of SEQ ID NO:2, or substitution, deletion or insertion of non-critical residues in non-critical regions of the protein. Non-functional allelic variants are naturally-occurring amino acid sequence variants of the 84569, e.g., human 84569, protein within a population that do not have the ability to attach a phosphate group to an 84569 ligand. Non-functional allelic variants will

typically contain a non-conservative substitution, a deletion, or insertion, or premature truncation of the amino acid sequence of SEQ ID NO:2, or a substitution, insertion, or deletion in critical residues or critical regions of the protein.

[0090] Moreover, nucleic acid molecules encoding other 84569 family members and, thus, which have a nucleotide sequence which differs from the 84569 sequences of SEQ ID NO:1 or SEQ ID NO:3 are intended to be within the scope of the invention.

Antisense Nucleic Acid Molecules, Ribozymes and Modified 84569 Nucleic Acid Molecules

[0091] In another aspect, the invention features, an isolated nucleic acid molecule which is antisense to 84569. An "antisense" nucleic acid can include a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. The antisense nucleic acid can be complementary to an entire 84569 coding strand, or to only a portion thereof (e.g., the coding region of human 84569 corresponding to SEQ ID NO:3). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding 84569 (e.g., the 5' and 3' untranslated regions).

[0092] An antisense nucleic acid can be designed such that it is complementary to the entire coding region of 84569 mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of 84569 mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of 84569 mRNA, e.g., between the -10 and +10 regions of the target gene nucleotide sequence of interest. An antisense oligonucleotide can be, for example, about 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or more nucleotides in length.

[0093] An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. The antisense nucleic acid also can be

produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

[0094] The antisense nucleic acid molecules of the invention are typically administered to a subject (e.g., by direct injection at a tissue site), or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an 84569 protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

[0095] In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier et al., (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue et al., (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., (1987) *FEBS Lett.* 215:327-330).

[0096] In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. A ribozyme having specificity for an 84569-encoding nucleic acid can include one or more sequences complementary to the nucleotide sequence of an 84569 cDNA disclosed herein (i.e., SEQ ID NO:1, or SEQ ID NO:3), and a sequence having known catalytic sequence responsible for mRNA cleavage (see U.S. Pat. No. 5,093,246 or Haselhoff and Gerlach, (1988) *Nature* 334:585-591). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an 84569-encoding mRNA. See, e.g., Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No.

5,116,742. Alternatively, 84569 mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

[0097] 84569 gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the 84569 (e.g., the 84569 promoter and/or enhancers) to form triple helical structures that prevent transcription of the 84569 gene in target cells. See generally, Helene, C., (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. et al., (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J., (1992) *Bioassays* 14(12):807-15. The potential sequences that can be targeted for triple helix formation can be increased by creating a so-called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

[0098] The invention also provides detectably labeled oligonucleotide primer and probe molecules. Typically, such labels are chemiluminescent, fluorescent, radioactive, or colorimetric.

[0099] AN 84569 nucleic acid molecule can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acid molecules can be modified to generate peptide nucleic acids (see Hyrup B. et al., (1996) *Bioorganic & Medicinal Chemistry* 4 (1): 5-23). As used herein, the terms "peptide nucleic acid" or "PNA" refers to a nucleic acid mimic, e.g., a DNA mimic, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of a PNA can allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup B. et al., (1996) *supra*; Perry-O'Keefe et al., *Proc. Natl. Acad. Sci.* 93: 14670-675.

[00100] PNAs of 84569 nucleic acid molecules can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, for example, inducing transcription or translation arrest or inhibiting replication. PNAs of 84569 nucleic acid molecules can also be used in the analysis of single base pair mutations in a gene, (e.g., by PNA-directed PCR clamping);

as 'artificial restriction enzymes' when used in combination with other enzymes, (e.g., S1 nucleases (Hyrup B., (1996) *supra*)); or as probes or primers for DNA sequencing or hybridization (Hyrup B. et al., (1996) *supra*; Perry-O'Keefe *supra*).

[00101] In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., (1989) *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre et al., (1987) *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (See, e.g., Krol et al., (1988) *Bio-Techniques* 6:958-976) or intercalating agents. (See, e.g., Zon, (1988) *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, (e.g., a peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent).

[00102] The invention also includes molecular beacon oligonucleotide primer and probe molecules having at least one region which is complementary to an 84569 nucleic acid of the invention, two complementary regions one having a fluorophore and one a quencher such that the molecular beacon is useful for quantitating the presence of the 84569 nucleic acid of the invention in a sample. Molecular beacon nucleic acids are described, for example, in Lizardi et al., U.S. Patent No. 5,854,033; Nazarenko et al., U.S. Patent No. 5,866,336, and Livak et al., U.S. Patent 5,876,930.

Isolated 84569 Polypeptides

[00103] In another aspect, the invention features, an isolated 84569 protein, or fragment, e.g., a biologically active portion, for use as immunogens or antigens to raise or test (or more generally to bind) anti-84569 antibodies. 84569 protein can be isolated from cells or tissue sources using standard protein purification techniques. 84569 protein or fragments thereof can be produced by recombinant DNA techniques or synthesized chemically.

[00104] Polypeptides of the invention include those which arise as a result of the existence of multiple genes, alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events. The polypeptide can be expressed in systems, e.g., cultured cells, which result in substantially the same postranslational modifications present when expressed the polypeptide is expressed in a

native cell, or in systems which result in the alteration or omission of postranslational modifications, e.g., glycosylation or cleavage, present when expressed in a native cell.

[00105] In a preferred embodiment, an 84569 polypeptide has one or more of the following characteristics:

it has the ability to regulate, sense and/or transmit an extracellular signal into a cell;

it has the ability to interact with (*e.g.*, bind to) intracellular phosphate ion;

it has the ability to mobilize an intracellular molecule that participates in a signal transduction pathway (*e.g.*, adenylate cyclase or phosphatidylinositol 4,5-bisphosphate (PIP₂), inositol 1,4,5-triphosphate (IP₃));

it has the ability to regulate intracellular signaling pathways;

it has the ability to modulate cell proliferation, cell migration, differentiation and/or cell survival;

it has the ability to modulate function, survival, morphology, proliferation and/or differentiation of cells of tissues in which 84569 molecules are expressed, (*e.g.*, hypothalamus);

it has a molecular weight (*e.g.*, deduced molecular weight), amino acid composition or other physical characteristic of an 84569 protein of SEQ ID NO:2;

it has an overall sequence similarity (identity) of at least 60%, preferably at least 70%, more preferably at least 75, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or more, with a polypeptide of SEQ ID NO:2;

it has an N-terminal domain which is preferably about 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or higher, identical to a polypeptide of SEQ ID NO:2; or

it has a protein kinase domain which preferably has an overall sequence similarity of about 70%, 80%, 90% or 95% with amino acid residues 468-731 of SEQ ID NO:2.

[00106] In a preferred embodiment the 84569 protein, or fragment thereof, differs from the corresponding sequence in SEQ ID NO:2. In one embodiment it differs by at least one but by less than 15, 10 or 5 amino acid residues. In another it differs from the corresponding sequence in SEQ ID NO:2 by at least one residue but less than 20%, 15%, 10% or 5% of the residues in it differ from the corresponding sequence in SEQ ID NO:2. (If this comparison requires alignment the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.) The differences are, preferably, differences or changes at a non-essential residue or a conservative substitution. In a preferred embodiment the differences are not in the protein

kinase domain. In another preferred embodiment one or more differences are in non-active site residues, e.g. outside of the protein kinase domain.

[00107] Other embodiments include a protein that contain one or more changes in amino acid sequence, e.g., a change in an amino acid residue which is not essential for activity. Such 84569 proteins differ in amino acid sequence from SEQ ID NO:2, yet retain biological activity.

[00108] In one embodiment, a biologically active portion of an 84569 protein includes an protein kinase domain. In another embodiment, a biologically active portion of an 84569 protein includes an ATP binding domain. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native 84569 protein.

[00109] In a preferred embodiment, the 84569 protein has an amino acid sequence shown in SEQ ID NO:2. In other embodiments, the 84569 protein is substantially identical to SEQ ID NO:2. In yet another embodiment, the 84569 protein is substantially identical to SEQ ID NO:2 and retains the functional activity of the protein of SEQ ID NO:2, as described in detail above. Accordingly, in another embodiment, the 84569 protein is a protein which includes an amino acid sequence at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more identical to SEQ ID NO:2.

84569 Chimeric or Fusion Proteins

[00110] In another aspect, the invention provides 84569 chimeric or fusion proteins. As used herein, an 84569 "chimeric protein" or "fusion protein" includes an 84569 polypeptide linked to a non-84569 polypeptide. A "non-84569 polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the 84569 protein, e.g., a protein which is different from the 84569 protein and which is derived from the same or a different organism. The 84569 polypeptide of the fusion protein can correspond to all or a portion e.g., a fragment described herein of an 84569 amino acid sequence. In a preferred embodiment, an 84569 fusion protein includes at least one (or two) biologically active portion of an 84569 protein. The non-84569 polypeptide can be fused to the N-terminus or C-terminus of the 84569 polypeptide.

[00111] The fusion protein can include a moiety which has a high affinity for a ligand. For example, the fusion protein can be a GST-84569 fusion protein in which the 84569 sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can

facilitate the purification of recombinant 84569. Alternatively, the fusion protein can be an 84569 protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of 84569 can be increased through use of a heterologous signal sequence.

[00112] Fusion proteins can include all or a part of a serum protein, e.g., an IgG constant region, or human serum albumin.

[00113] The 84569 fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject *in vivo*. The 84569 fusion proteins can be used to affect the bioavailability of an 84569 substrate. 84569 fusion proteins may be useful therapeutically for the treatment of disorders caused by, for example, (i) aberrant modification or mutation of a gene encoding an 84569 protein; (ii) mis-regulation of the 84569 gene; and (iii) aberrant post-translational modification of an 84569 protein.

[00114] Moreover, the 84569-fusion proteins of the invention can be used as immunogens to produce anti-84569 antibodies in a subject, to purify 84569 ligands and in screening assays to identify molecules which inhibit the interaction of 84569 with an 84569 substrate.

[00115] Expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). AN 84569-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the 84569 protein.

Variants of 84569 Proteins

[00116] In another aspect, the invention also features a variant of an 84569 polypeptide, e.g., which functions as an agonist (mimetics) or as an antagonist. Variants of the 84569 proteins can be generated by mutagenesis, e.g., discrete point mutation, the insertion or deletion of sequences or the truncation of an 84569 protein. An agonist of the 84569 proteins can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of an 84569 protein. An antagonist of an 84569 protein can inhibit one or more of the activities of the naturally occurring form of the 84569 protein by, for example, competitively modulating an 84569-mediated activity of an 84569 protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Preferably, treatment of a subject with a variant having a subset of the biological activities

of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the 84569 protein.

[00117] Variants of an 84569 protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of an 84569 protein for agonist or antagonist activity.

[00118] Libraries of fragments e.g., N terminal, C terminal, or internal fragments, of an 84569 protein coding sequence can be used to generate a variegated population of fragments for screening and subsequent selection of variants of an 84569 protein.

[00119] Variants in which a cysteine residues is added or deleted or in which a residue which is glycosylated is added or deleted are particularly preferred.

[00120] Methods for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify 84569 variants (Arkin and Yourvan, (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave et al., (1993) *Protein Engineering* 6(3):327-331).

[00121] Cell based assays can be exploited to analyze a variegated 84569 library. For example, a library of expression vectors can be transfected into a cell line, e.g., a cell line, which ordinarily responds to 84569 in a substrate-dependent manner. The transfected cells are then contacted with 84569 and the effect of the expression of the mutant on signaling by the 84569 substrate can be detected, e.g., by measuring protein kinase activity. Plasmid DNA can then be recovered from the cells which score for inhibition, or alternatively, potentiation of signaling by the 84569 substrate, and the individual clones further characterized.

[00122] In another aspect, the invention features a method of making an 84569 polypeptide, e.g., a peptide having a non-wild type activity, e.g., an antagonist, agonist, or super agonist of a naturally occurring 84569 polypeptide, e.g., a naturally occurring 84569 polypeptide. The method includes: altering the sequence of an 84569 polypeptide, e.g., altering the sequence, e.g., by substitution or deletion of one or more residues of a non-conserved region, a domain or residue disclosed herein, and testing the altered polypeptide for the desired activity.

[00123] In another aspect, the invention features a method of making a fragment or analog of an 84569 polypeptide a biological activity of a naturally occurring 84569

polypeptide. The method includes: altering the sequence, e.g., by substitution or deletion of one or more residues, of an 84569 polypeptide, e.g., altering the sequence of a non-conserved region, or a domain or residue described herein, and testing the altered polypeptide for the desired activity.

Anti-84569 Antibodies

[00124] In another aspect, the invention provides an anti-84569 antibody. The term "antibody" as used herein refers to an immunoglobulin molecule or immunologically active portion thereof, i.e., an antigen-binding portion. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin.

[00125] The antibody can be a polyclonal, monoclonal, recombinant, e.g., a chimeric or humanized, fully human, non-human, e.g., murine, or single chain antibody. In a preferred embodiment it has effector function and can fix complement. The antibody can be coupled to a toxin or imaging agent.

[00126] A full-length 84569 protein or, antigenic peptide fragment of 84569 can be used as an immunogen or can be used to identify anti-84569 antibodies made with other immunogens, e.g., cells, membrane preparations, and the like. The antigenic peptide of 84569 should include at least 8 amino acid residues of the amino acid sequence shown in SEQ ID NO:2 and encompasses an epitope of 84569. Preferably, the antigenic peptide includes at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues.

[00127] Fragments of 84569 which include, e.g., residues 468-731 of SEQ ID NO:2 can be used to make an antibody against the protein kinase region of the 84569 protein. Antibodies reactive with, or specific for, any of these regions, or other regions or domains described herein are provided.

[00128] In a preferred embodiment the antibody fails to bind an Fc receptor, e.g. it is a type which does not support Fc receptor binding or has been modified, e.g., by deletion or other mutation, such that it does not have a functional Fc receptor binding region.

[00129] Preferred epitopes encompassed by the antigenic peptide are regions of 84569 are located on the surface of the protein, e.g., hydrophilic regions, as well as regions with high antigenicity. For example, an Emini surface probability analysis of the human 84569

protein sequence can be used to indicate the regions that have a particularly high probability of being localized to the surface of the 84569 protein and are thus likely to constitute surface residues useful for targeting antibody production.

[00130] In a preferred embodiment the antibody binds an epitope on any domain or region on 84569 proteins described herein.

[00131] Chimeric, humanized, but most preferably, completely human antibodies are desirable for applications which include repeated administration, e.g., therapeutic treatment (and some diagnostic applications) of human patients.

[00132] The anti-84569 antibody can be a single chain antibody. A single-chain antibody (scFV) may be engineered (see, for example, Colcher, D. et al., *Ann. NY Acad. Sci.* 1999 Jun 30;880:263-80; and Reiter, Y., *Clin. Cancer Res.* 1996 Feb;2(2):245-52). The single chain antibody can be dimerized or multimerized to generate multivalent antibodies having specificities for different epitopes of the same target 84569 protein.

[00133] An anti-84569 antibody (e.g., monoclonal antibody) can be used to isolate 84569 by standard techniques, such as affinity chromatography or immunoprecipitation.

Moreover, an anti-84569 antibody can be used to detect 84569 protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the protein. Anti-84569 antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance (i.e., antibody labeling). Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Recombinant Expression Vectors, Host Cells and Genetically Engineered Cells

[00134] In another aspect, the invention includes, vectors, preferably expression vectors, containing a nucleic acid encoding a polypeptide described herein. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked and can include a plasmid, cosmid or viral vector. The vector can be capable of autonomous replication or it can integrate into a host DNA. Viral vectors include, e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses.

[00135] A vector can include an 84569 nucleic acid in a form suitable for expression of the nucleic acid in a host cell. Preferably the recombinant expression vector includes one or more regulatory sequences operatively linked to the nucleic acid sequence to be expressed. The term "regulatory sequence" includes promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence, as well as tissue-specific regulatory and/or inducible sequences. The design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or polypeptides, including fusion proteins or polypeptides, encoded by nucleic acids as described herein (e.g., 84569 proteins, mutant forms of 84569 proteins, fusion proteins, and the like).

[00136] The recombinant expression vectors of the invention can be designed for expression of 84569 proteins in prokaryotic or eukaryotic cells. For example, polypeptides of the invention can be expressed in *E. coli*, insect cells (e.g., using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

[00137] Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, a proteolytic

cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S., (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

[00138] Purified fusion proteins can be used in 84569 activity assays, (e.g., direct assays or competitive assays described in detail below), or to generate antibodies specific for 84569 proteins. In a preferred embodiment, a fusion protein expressed in a retroviral expression vector of the present invention can be used to infect bone marrow cells which are subsequently transplanted into irradiated recipients. The pathology of the subject recipient is then examined after sufficient time has passed (e.g., six (6) weeks).

[00139] To maximize recombinant protein expression in *E. coli* is to express the protein in host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada et al., (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

[00140] The 84569 expression vector can be a yeast expression vector, a vector for expression in insect cells, e.g., a baculovirus expression vector or a vector suitable for expression in mammalian cells.

[00141] When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40.

[00142] In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert et al., (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and

Eaton, (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji et al., (1983) *Cell* 33:729-740; Queen and Baltimore, (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, (1989) *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund et al., (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166).

Developmentally-regulated promoters are also encompassed, for example, the murine hox promoters (Kessel and Gruss, (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman, (1989) *Genes Dev.* 3:537-546).

[00143] The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. Regulatory sequences (e.g., viral promoters and/or enhancers) operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the constitutive, tissue specific or cell type specific expression of antisense RNA in a variety of cell types. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. et al., Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

[00144] Another aspect the invention provides a host cell which includes a nucleic acid molecule described herein, e.g., an 84569 nucleic acid molecule within a recombinant expression vector or an 84569 nucleic acid molecule containing sequences which allow it to homologously recombine into a specific site of the host cell's genome. The terms "host cell" and "recombinant host cell" are used interchangeably herein. Such terms refer not only to the particular subject cell but rather also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[00145] A host cell can be any prokaryotic or eukaryotic cell. For example, an 84569 protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

[00146] Vector DNA can be introduced into host cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation

[00147] A host cell of the invention can be used to produce (i.e., express) an 84569 protein. Accordingly, the invention further provides methods for producing an 84569 protein using the host cells of the invention. In one embodiment, the method includes culturing the host cell of the invention (into which a recombinant expression vector encoding an 84569 protein has been introduced) in a suitable medium such that an 84569 protein is produced. In another embodiment, the method further includes isolating an 84569 protein from the medium or the host cell.

[00148] In another aspect, the invention features, a cell or purified preparation of cells which include an 84569 transgene, or which otherwise misexpress 84569. The cell preparation can consist of human or non-human cells, e.g., rodent cells, e.g., mouse or rat cells, rabbit cells, or pig cells. In preferred embodiments, the cell or cells include an 84569 transgene, e.g., a heterologous form of an 84569, e.g., a gene derived from humans (in the case of a non-human cell). The 84569 transgene can be misexpressed, e.g., overexpressed or underexpressed. In other preferred embodiments, the cell or cells include a gene which misexpress an endogenous 84569, e.g., a gene the expression of which is disrupted, e.g., a knockout. Such cells can serve as a model for studying disorders which are related to mutated or mis-expressed 84569 alleles or for use in drug screening.

[00149] In another aspect, the invention features, a human cell, e.g., a neural stem cell, transformed with nucleic acid which encodes a subject 84569 polypeptide.

[00150] Also provided are cells or a purified preparation thereof, e.g., human cells, in which an endogenous 84569 is under the control of a regulatory sequence that does not normally control the expression of the endogenous 84569 gene. The expression characteristics of an endogenous gene within a cell, e.g., a cell line or microorganism, can be modified by inserting a heterologous DNA regulatory element into the genome of the cell such that the inserted regulatory element is operably linked to the endogenous 84569 gene. For example, an endogenous 84569 gene, e.g., a gene which is "transcriptionally silent," e.g., not normally expressed, or expressed only at very low levels, may be activated by inserting a regulatory element which is capable of promoting the expression of a normally

expressed gene product in that cell. Techniques such as targeted homologous recombinations, can be used to insert the heterologous DNA as described in, e.g., Chappel, US 5,272,071; WO 91/06667, published on May 16, 1991.

Transgenic Animals

[00151] The invention provides non-human transgenic animals. Such animals are useful for studying the function and/or activity of an 84569 protein and for identifying and/or evaluating modulators of 84569 activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, and the like. A transgene is exogenous DNA or a rearrangement, e.g., a deletion of endogenous chromosomal DNA, which preferably is integrated into or occurs in the genome of the cells of a transgenic animal. A transgene can direct the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal, other transgenes, e.g., a knockout, reduce expression. Thus, a transgenic animal can be one in which an endogenous 84569 gene has been altered by, e.g., by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

[00152] Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to a transgene of the invention to direct expression of an 84569 protein to particular cells. A transgenic founder animal can be identified based upon the presence of an 84569 transgene in its genome and/or expression of 84569 mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding an 84569 protein can further be bred to other transgenic animals carrying other transgenes.

[00153] 84569 proteins or polypeptides can be expressed in transgenic animals or plants, e.g., a nucleic acid encoding the protein or polypeptide can be introduced into the genome of an animal. In preferred embodiments the nucleic acid is placed under the control of a tissue specific promoter, e.g., a milk or egg specific promoter, and recovered from the milk or eggs produced by the animal. Suitable animals are mice, pigs, cows, goats, and sheep.

[00154] The invention also includes a population of cells from a transgenic animal, as discussed herein.

Uses and Methods of the Invention

[00155] The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: a) screening assays; b) predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenetics); and c) methods of treatment (e.g., therapeutic and prophylactic). In particularly preferred embodiments, the compositions provided herein are used in conjunction with methods of diagnosis and treatment of metabolic disorders (e.g., obesity, hyperlipidemia, diabetes, anorexia, and cachexia).

[00156] The isolated nucleic acid molecules of the invention can be used, for example, to express an 84569 protein (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect an 84569 mRNA (e.g., in a biological sample such as adipose tissue) or a genetic alteration in an 84569 gene, and to modulate 84569 activity, as described further below. The 84569 proteins can be used to treat disorders characterized by insufficient or excessive production of an 84569 substrate or production of 84569 inhibitors (e.g., a metabolic disorder). In addition, the 84569 proteins can be used to screen for naturally occurring 84569 substrates, to screen for drugs or compounds which modulate 84569 activity, as well as to treat disorders characterized by insufficient or excessive production of 84569 protein or production of 84569 protein forms which have decreased, aberrant or unwanted activity compared to 84569 wild-type protein. Such disorders include those characterized by aberrant signaling or aberrant, e.g., hyperproliferative, cell growth. Moreover, the anti-84569 antibodies of the invention can be used to detect and isolate 84569 proteins, regulate the bioavailability of 84569 proteins, and modulate 84569 activity.

[00157] A method of evaluating a compound for the ability to interact with, e.g., bind, a subject 84569 polypeptide is provided. The method includes: contacting the compound with the subject 84569 polypeptide; and evaluating ability of the compound to interact with, e.g., to bind or form a complex with the subject 84569 polypeptide. This method can be performed *in vitro*, e.g., in a cell free system, or *in vivo*, e.g., in a two-hybrid interaction trap assay. This method can be used to identify naturally occurring molecules which interact

with subject 84569 polypeptide. It can also be used to find natural or synthetic inhibitors of subject 84569 polypeptide. Screening methods are discussed in more detail below.

Screening Assays:

[00158] The invention provides methods (also referred to herein as "screening assays") for identifying modulators, i.e., candidate or test compounds or agents (e.g., proteins, peptides, peptidomimetics, peptoids, small molecules or other drugs) which bind to 84569 proteins, have a stimulatory or inhibitory effect on, for example, 84569 expression or 84569 activity, or have a stimulatory or inhibitory effect on, for example, the expression or activity of an 84569 substrate. Compounds thus identified can be used to modulate the activity of target gene products (e.g., 84569 genes) in a therapeutic protocol, to elaborate the biological function of the target gene product, or to identify compounds that disrupt normal target gene interactions.

[00159] In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of an 84569 protein or polypeptide or a biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of an 84569 protein or polypeptide or a biologically active portion thereof.

[00160] The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries [libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive] (see, e.g., Zuckermann, R.N. et al., *J. Med. Chem.* 1994, 37: 2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

[00161] Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.*, (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.*, (1994). *J. Med. Chem.* 37:2678; Cho *et al.*, (1993) *Science* 261:1303; Carrell *et al.*, (1994) *Angew. Chem. Int. Ed.*

Engl. 33:2059; Carell et al., (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop et al., (1994) *J. Med. Chem.* 37:1233.

[00162] Libraries of compounds may be presented in solution (e.g., Houghten, (1992) *Biotechniques* 13:412-421), or on beads (Lam, (1991) *Nature* 354:82-84), chips (Fodor, (1993) *Nature* 364:555-556), bacteria or spores (Ladner, United States Patent No. 5,223,409), plasmids (Cull et al., (1992) *Proc. Natl. Acad. Sci. USA* 89:1865-1869) or on phage (Scott and Smith, (1990) *Science* 249:386-390); (Devlin, (1990) *Science* 249:404-406); (Cwirla et al., (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382); (Felici, (1991) *J. Mol. Biol.* 222:301-310); (Ladner *supra.*).

[00163] In one embodiment, an assay is a cell-based assay in which a cell which expresses an 84569 protein or biologically active portion thereof is contacted with a test compound, and the ability of the test compound to modulate 84569 activity is determined. Determining the ability of the test compound to modulate 84569 activity can be accomplished by monitoring, for example, protein kinase activity. The cell, for example, can be of mammalian origin, e.g., human. Cell homogenates, or fractions, preferably membrane containing fractions, can also be tested.

[00164] The ability of the test compound to modulate 84569 binding to a compound, e.g., an 84569 substrate, or to bind to 84569 can also be evaluated. This can be accomplished, for example, by coupling the compound, e.g., the substrate, with a radioisotope or enzymatic label such that binding of the compound, e.g., the substrate, to 84569 can be determined by detecting the labeled compound, e.g., substrate, in a complex. Alternatively, 84569 could be coupled with a radioisotope or enzymatic label to monitor the ability of a test compound to modulate 84569 binding to an 84569 substrate in a complex. For example, compounds (e.g., 84569 substrates) can be labeled with ¹²⁵I, ³⁵S, ¹⁴C, or ³H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

[00165] The ability of the 84569 protein to phosphorylate an 84569 target molecule can be determined by, for example, an *in vitro* kinase assay. Briefly, an 84569 target molecule, e.g., an immunoprecipitated 84569 target molecule from a cell line expressing such a molecule, can be incubated with the 84569 protein and radioactive ATP, e.g., [γ -³²P] ATP,

in a buffer containing MgCl_2 and MnCl_2 , e.g., 10 mM MgCl_2 and 5 mM MnCl_2 .

Following the incubation, the immunoprecipitated 84569 target molecule can be separated by SDS-polyacrylamide gel electrophoresis under reducing conditions, transferred to a membrane, e.g., a PVDF membrane, and autoradiographed. The appearance of detectable bands on the autoradiograph indicates that the 84569 substrate has been phosphorylated. Phosphoaminoacid analysis of the phosphorylated substrate can also be performed in order to determine which residues on the 84569 substrate are phosphorylated. Briefly, the radiophosphorylated protein band can be excised from the SDS gel and subjected to partial acid hydrolysis. The products can then be separated by one-dimensional electrophoresis and analyzed on, for example, a phosphoimager and compared to ninhydrin-stained phosphoaminoacid standards.

[00166] The ability of a compound (e.g., an 84569 substrate) to interact with 84569 with or without the labeling of any of the interactants can be evaluated. For example, a microphysiometer can be used to detect the interaction of a compound with 84569 without the labeling of either the compound or the 84569. McConnell, H. M. et al., (1992) *Science* 257:1906-1912. As used herein, a "microphysiometer" (e.g., Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a compound and 84569.

[00167] In yet another embodiment, a cell-free assay is provided in which an 84569 protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to bind to the 84569 protein or biologically active portion thereof is evaluated. Preferred biologically active portions of the 84569 proteins to be used in assays of the present invention include fragments which participate in interactions with non-84569 molecules, e.g., fragments with high surface probability scores.

[00168] Soluble and/or membrane-bound forms of isolated proteins (e.g., 84569 proteins or biologically active portions thereof) can be used in the cell-free assays of the invention. When membrane-bound forms of the protein are used, it may be desirable to utilize a solubilizing agent. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane

sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate.

[00169] Cell-free assays involve preparing a reaction mixture of the target gene protein and the test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex that can be removed and/or detected.

[00170] In one embodiment, assays are performed where the ability of an agent to block protein kinase activity within a cell is evaluated.

[00171] The interaction between two molecules can also be detected, e.g., using fluorescence energy transfer (FET) (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, et al., U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, the spatial relationship between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (e.g., using a fluorimeter).

[00172] In another embodiment, determining the ability of the 84569 protein to bind to a target molecule can be accomplished using real-time Biomolecular Interaction Analysis (BIA) (see, e.g., Sjolander, S. and Urbaniczky, C., (1991) *Anal. Chem.* **63**:2338-2345 and Szabo et al., (1995) *Curr. Opin. Struct. Biol.* **5**:699-705). "Surface plasmon resonance" or "BIA" detects biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

[00173] In one embodiment, the target gene product or the test substance is anchored onto a solid phase. The target gene product/test compound complexes anchored on the solid

phase can be detected at the end of the reaction. Preferably, the target gene product can be anchored onto a solid surface, and the test compound, (which is not anchored), can be labeled, either directly or indirectly, with detectable labels discussed herein.

[00174] It may be desirable to immobilize either 84569, an anti-84569 antibody or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to an 84569 protein, or interaction of an 84569 protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase/84569 fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or 84569 protein, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of 84569 binding or activity determined using standard techniques.

[00175] Other techniques for immobilizing either an 84569 protein or a target molecule on matrices include using conjugation of biotin and streptavidin. Biotinylated 84569 protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical).

[00176] In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously

non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the immobilized component (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody).

[00177] In one embodiment, this assay is performed utilizing antibodies reactive with 84569 protein or target molecules but which do not interfere with binding of the 84569 protein to its target molecule. Such antibodies can be derivatized to the wells of the plate, and unbound target or 84569 protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the 84569 protein or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the 84569 protein or target molecule.

[00178] Alternatively, cell free assays can be conducted in a liquid phase. In such an assay, the reaction products are separated from unreacted components, by any of a number of standard techniques, including but not limited to: differential centrifugation (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993 Aug;18(8):284-7); chromatography (gel filtration chromatography, ion-exchange chromatography); electrophoresis (see, e.g., Ausubel, F. et al., eds. *Current Protocols in Molecular Biology* 1999, J. Wiley: New York.); and immunoprecipitation (see, for example, Ausubel, F. et al., eds. *Current Protocols in Molecular Biology* 1999, J. Wiley: New York). Such resins and chromatographic techniques are known to one skilled in the art (see, e.g., Heegaard, N.H., *J Mol. Recognit.* 1998 Winter;11(1-6):141-8; Hage, D.S., and Tweed, S.A., *J. Chromatogr. B Biomed. Sci. Appl.* 1997 Oct 10;699(1-2):499-525). Further, fluorescence energy transfer may also be conveniently utilized, as described herein, to detect binding without further purification of the complex from solution.

[00179] In a preferred embodiment, the assay includes contacting the 84569 protein or biologically active portion thereof with a known compound which binds 84569 to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an 84569 protein, wherein determining the ability of the test compound to interact with an 84569 protein includes determining the ability of the test compound to preferentially bind to 84569 or biologically active portion thereof, or to modulate the activity of a target molecule, as compared to the known compound.

[00180] The target gene products of the invention can, *in vivo*, interact with one or more cellular or extracellular macromolecules, such as proteins. For the purposes of this discussion, such cellular and extracellular macromolecules are referred to herein as "binding partners." Compounds that disrupt such interactions can be useful in regulating the activity of the target gene product. Such compounds can include, but are not limited to molecules such as antibodies, peptides, and small molecules. The preferred target genes/products for use in this embodiment are the 84569 genes herein identified. In an alternative embodiment, the invention provides methods for determining the ability of the test compound to modulate the activity of an 84569 protein through modulation of the activity of a downstream effector of an 84569 target molecule. For example, the activity of the effector molecule on an appropriate target can be determined, or the binding of the effector to an appropriate target can be determined, as previously described.

[00181] To identify compounds that interfere with the interaction between the target gene product and its cellular or extracellular binding partner(s), e.g., a substrate, a reaction mixture containing the target gene product and the binding partner is prepared, under conditions and for a time sufficient, to allow the two products to form complex. In order to test an inhibitory agent, the reaction mixture is provided in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the target gene and its cellular or extracellular binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the target gene product and the cellular or extracellular binding partner is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the target gene product and the interactive binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal target gene product can also be compared to complex formation within reaction mixtures containing the test compound and mutant target gene product. This comparison can be important in those cases wherein it is desirable to identify compounds that disrupt interactions of mutant but not normal target gene products.

[00182] These assays can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the target gene product or the binding partner onto a solid phase, and detecting complexes anchored on the solid phase at the end

of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the target gene products and the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance. Alternatively, test compounds that disrupt preformed complexes, e.g., compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

[00183] In a heterogeneous assay system, either the target gene product or the interactive cellular or extracellular binding partner, is anchored onto a solid surface (e.g., a microtiter plate), while the non-anchored species is labeled, either directly or indirectly. The anchored species can be immobilized by non-covalent or covalent attachments. Alternatively, an immobilized antibody specific for the species to be anchored can be used to anchor the species to the solid surface.

[00184] In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds that inhibit complex formation or that disrupt preformed complexes can be detected.

[00185] Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds that inhibit complex or that disrupt preformed complexes can be identified.

[00186] In an alternate embodiment of the invention, a homogeneous assay can be used. For example, a preformed complex of the target gene product and the interactive cellular or extracellular binding partner product is prepared in that either the target gene products or their binding partners are labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 that utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt target gene product-binding partner interaction can be identified.

[00187] In yet another aspect, the 84569 proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos et al., (1993) *Cell* 72:223-232; Madura et al., (1993) *J. Biol. Chem.* 268:12046-12054; Bartel et al., (1993) *Biotechniques* 14:920-924; Iwabuchi et al., (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins, which bind to or interact with 84569 ("84569-binding proteins" or "84569-bp") and are involved in 84569 activity. Such 84569-bps can be activators or inhibitors of signals by the 84569 proteins or 84569 targets as, for example, downstream elements of an 84569-mediated signaling pathway.

[00188] The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for an 84569 protein is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. (Alternatively the: 84569 protein can be the fused to the activator domain.) If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an 84569-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the 84569 protein.

[00189] In another embodiment, modulators of 84569 expression are identified. For example, a cell or cell free mixture is contacted with a candidate compound and the expression of 84569 mRNA or protein evaluated relative to the level of expression of 84569 mRNA or protein in the absence of the candidate compound. When expression of 84569 mRNA or protein is greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of 84569 mRNA or protein expression. Alternatively, when expression of 84569 mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of 84569 mRNA or protein expression. The level of 84569 mRNA or protein expression can be determined by methods described herein for detecting 84569 mRNA or protein.

[00190] In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of an 84569 protein can be confirmed *in vivo*, e.g., in an animal.

[00191] This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein (e.g., an 84569 modulating agent, an antisense 84569 nucleic acid molecule, an 84569-specific antibody, or an 84569-binding partner) in an appropriate animal model to determine the efficacy, toxicity, side effects, or mechanism of action, of treatment with such an agent. Furthermore, novel agents identified by the above-described screening assays can be used for treatments as described herein.

Detection Assays

[00192] Portions or fragments of the nucleic acid sequences identified herein can be used as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome e.g., to locate gene regions associated with genetic disease or to associate 84569 with a disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. These applications are described in the subsections below.

Chromosome Mapping

[00193] The 84569 nucleotide sequences or portions thereof can be used to map the location of the 84569 genes on a chromosome. This process is called chromosome mapping. Chromosome mapping is useful in correlating the 84569 sequences with genes associated with disease.

[00194] Briefly, 84569 genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the 84569 nucleotide sequences. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the 84569 sequences will yield an amplified fragment.

[00195] A panel of somatic cell hybrids in which each cell line contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, can allow easy mapping of individual genes to specific human chromosomes. (D'Eustachio P. et al., (1983) *Science* 220:919-924).

[00196] Other mapping strategies e.g., in situ hybridization (described in Fan, Y. et al., (1990) *Proc. Natl. Acad. Sci. USA*, 87:6223-27), pre-screening with labeled flow-sorted chromosomes, and pre-selection by hybridization to chromosome specific cDNA libraries can be used to map 84569 to a chromosomal location.

[00197] Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases will suffice to get good results at a reasonable amount of time. For a review of this technique, see Verma et al., *Human Chromosomes: A Manual of Basic Techniques* (Pergamon Press, New York 1988).

[00198] Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

[00199] Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, Mendelian Inheritance in Man, available on-line through Johns Hopkins University Welch Medical Library). The relationship between a gene and a disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, for example, Egeland, J. et al., (1987) *Nature*, 325:783-787.

[00200] Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the 84569 gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

[00201] 84569 sequences can be used to identify individuals from biological samples using, e.g., restriction fragment length polymorphism (RFLP). In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, the fragments separated, e.g., in a Southern blot, and probed to yield bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP (described in U.S. Patent 5,272,057).

[00202] Furthermore, the sequences of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the 84569 nucleotide sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it. Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences.

[00203] Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:1 can provide positive individual identification with a panel of perhaps 10 to 1,000 primers which each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NO:3 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

[00204] If a panel of reagents from 84569 nucleotide sequences described herein is used to generate a unique identification database for an individual, those same reagents can later be used to identify tissue from that individual. Using the unique identification database, positive identification of the individual, living or dead, can be made from extremely small tissue samples.

Use of Partial 84569 Sequences in Forensic Biology

[00205] DNA-based identification techniques can also be used in forensic biology. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

[00206] The sequences of the present invention can be used to provide polynucleotide reagents, e.g., PCR primers, targeted to specific loci in the human genome, which can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (i.e. another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NO:1 (e.g., fragments derived from the noncoding regions of SEQ ID NO:1 having a length of at least 20 bases, preferably at least 30 bases) are particularly appropriate for this use.

[00207] The 84569 nucleotide sequences described herein can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes which can be used in, for example,

an *in situ* hybridization technique, to identify a specific tissue, e.g., a tissue containing protein kinase activity. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such 84569 probes can be used to identify tissue by species and/or by organ type.

[00208] In a similar fashion, these reagents, e.g., 84569 primers or probes can be used to screen tissue culture for contamination (i.e. screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

[00209] The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual.

[00210] Generally, the invention provides, a method of determining if a subject is at risk for a disorder related to a lesion in or the misexpression of a gene which encodes 84569.

[00211] Such disorders include, e.g., a disorder associated with the misexpression of 84569, or lipid metabolism related disorder.

[00212] The method includes one or more of the following:

detecting, in a tissue of the subject, the presence or absence of a mutation which affects the expression of the 84569 gene, or detecting the presence or absence of a mutation in a region which controls the expression of the gene, e.g., a mutation in the 5' control region;

detecting, in a tissue of the subject, the presence or absence of a mutation which alters the structure of the 84569 gene;

detecting, in a tissue of the subject, the misexpression of the 84569 gene, at the mRNA level, e.g., detecting a non-wild type level of a mRNA ;

detecting, in a tissue of the subject, the misexpression of the gene, at the protein level, e.g., detecting a non-wild type level of an 84569 polypeptide.

[00213] In preferred embodiments the method includes: ascertaining the existence of at least one of: a deletion of one or more nucleotides from the 84569 gene; an insertion of one or more nucleotides into the gene, a point mutation, e.g., a substitution of one or more nucleotides of the gene, a gross chromosomal rearrangement of the gene, e.g., a translocation, inversion, or deletion.

[00214] For example, detecting the genetic lesion can include: (i) providing a probe/primer including an oligonucleotide containing a region of nucleotide sequence which

hybridizes to a sense or antisense sequence from SEQ ID NO:1 naturally occurring mutants thereof or 5' or 3' flanking sequences naturally associated with the 84569 gene; (ii) exposing the probe/primer to nucleic acid of the tissue; and detecting, by hybridization, e.g., *in situ* hybridization, of the probe/primer to the nucleic acid, the presence or absence of the genetic lesion.

[00215] In preferred embodiments detecting the misexpression includes ascertaining the existence of at least one of: an alteration in the level of a messenger RNA transcript of the 84569 gene; the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene; or a non-wild type level of 84569.

[00216] Methods of the invention can be used prenatally or to determine if a subject's offspring will be at risk for a disorder.

[00217] In preferred embodiments the method includes determining the structure of an 84569 gene, an abnormal structure being indicative of risk for the disorder.

[00218] In preferred embodiments the method includes contacting a sample from the subject with an antibody to the 84569 protein or a nucleic acid, which hybridizes specifically with the gene. These and other embodiments are discussed below.

Diagnostic and Prognostic Assays

[00219] The presence, level, or absence of 84569 protein or nucleic acid in a biological sample can be evaluated by obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting 84569 protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes 84569 protein such that the presence of 84569 protein or nucleic acid is detected in the biological sample. The term "biological sample" includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. A preferred biological sample is serum. The level of expression of the 84569 gene can be measured in a number of ways, including, but not limited to: measuring the mRNA encoded by the 84569 genes; measuring the amount of protein encoded by the 84569 genes; or measuring the activity of the protein encoded by the 84569 genes.

[00220] The level of mRNA corresponding to the 84569 gene in a cell can be determined both by *in situ* and by *in vitro* formats.

[00221] The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction

analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length 84569 nucleic acid, such as the nucleic acid of SEQ ID NO:1 or SEQ ID NO:3, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250, 500, 750, 1000, 1250, 1500, 1600, 1700, 1800, 1900, 2000, nucleotides in length and sufficient to specifically hybridize under stringent conditions to 84569 mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays are described herein.

[00222] In one format, mRNA (or cDNA) is immobilized on a surface and contacted with the probes, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probes are immobilized on a surface and the mRNA (or cDNA) is contacted with the probes, for example, in a two-dimensional gene chip array. A skilled artisan can adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the 84569 genes.

[00223] The level of mRNA in a sample that is encoded by one of 84569 can be evaluated with nucleic acid amplification, e.g., by rtPCR (Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA* 88:189-193), self sustained sequence replication (Guatelli et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh et al., 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi et al., 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi et al., U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques known in the art. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

[00224] For *in situ* methods, a cell or tissue sample can be prepared/processed and immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the 84569 gene being analyzed.

[00225] In another embodiment, the methods further contacting a control sample with a compound or agent capable of detecting 84569 mRNA, or genomic DNA, and comparing the presence of 84569 mRNA or genomic DNA in the control sample with the presence of 84569 mRNA or genomic DNA in the test sample.

[00226] A variety of methods can be used to determine the level of protein encoded by 84569. In general, these methods include contacting an agent that selectively binds to the protein, such as an antibody with a sample, to evaluate the level of protein in the sample. In a preferred embodiment, the antibody bears a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with a detectable substance. Examples of detectable substances are provided herein.

[00227] The detection methods can be used to detect 84569 protein in a biological sample *in vitro* as well as *in vivo*. *In vitro* techniques for detection of 84569 protein include enzyme linked immunosorbent assays (ELISAs), immunoprecipitations, immunofluorescence, enzyme immunoassay (EIA), radioimmunoassay (RIA), and Western blot analysis. *In vivo* techniques for detection of 84569 protein include introducing into a subject a labeled anti-84569 antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

[00228] In another embodiment, the methods further include contacting the control sample with a compound or agent capable of detecting 84569 protein, and comparing the presence of 84569 protein in the control sample with the presence of 84569 protein in the test sample.

[00229] The invention also includes kits for detecting the presence of 84569 in a biological sample. For example, the kit can include a compound or agent capable of detecting 84569 protein or mRNA in a biological sample; and a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect 84569 protein or nucleic acid.

[00230] For antibody-based kits, the kit can include: (1) a first antibody (e.g., attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention;

and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable agent.

[00231] For oligonucleotide-based kits, the kit can include: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide corresponding to a marker of the invention or (2) a pair of primers useful for amplifying a nucleic acid molecule corresponding to a marker of the invention. The kit can also include a buffering agent, a preservative, or a protein-stabilizing agent. The kit can also include components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample contained. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

[00232] The diagnostic methods described herein can identify subjects having, or at risk of developing, a disease or disorder associated with misexpressed or aberrant or unwanted 84569 expression or activity. As used herein, the term "unwanted" includes an unwanted phenomenon involved in a biological response such as pain or deregulated cell proliferation.

[00233] In one embodiment, a disease or disorder associated with aberrant or unwanted 84569 expression or activity is identified. A test sample is obtained from a subject and 84569 protein or nucleic acid (e.g., mRNA or genomic DNA) is evaluated, wherein the level, e.g., the presence or absence, of 84569 protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant or unwanted 84569 expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest, including a biological fluid (e.g., serum), cell sample, or tissue.

[00234] The prognostic assays described herein can be used to determine whether a subject can be administered an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant or unwanted 84569 expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a cellular growth related disorder.

[00235] The methods of the invention can also be used to detect genetic alterations in an 84569 gene, thereby determining if a subject with the altered gene is at risk for a disorder

characterized by misregulation in 84569 protein activity or nucleic acid expression, such as a cellular growth related disorder. In preferred embodiments, the methods include detecting, in a sample from the subject, the presence or absence of a genetic alteration characterized by at least one of an alteration affecting the integrity of a gene encoding an 84569-protein, or the mis-expression of the 84569 gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of 1) a deletion of one or more nucleotides from an 84569 gene; 2) an addition of one or more nucleotides to an 84569 gene; 3) a substitution of one or more nucleotides of an 84569 gene, 4) a chromosomal rearrangement of an 84569 gene; 5) an alteration in the level of a messenger RNA transcript of an 84569 gene, 6) aberrant modification of an 84569 gene, such as of the methylation pattern of the genomic DNA, 7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of an 84569 gene, 8) a non-wild type level of an 84569-protein, 9) allelic loss of an 84569 gene, and 10) inappropriate post-translational modification of an 84569-protein.

[00236] An alteration can be detected without a probe/primer in a polymerase chain reaction, such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR), the latter of which can be particularly useful for detecting point mutations in the 84569-gene. This method can include the steps of collecting a sample of cells from a subject, isolating nucleic acid (e.g., genomic, mRNA or both) from the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to an 84569 gene under conditions such that hybridization and amplification of the 84569-gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

[00237] Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. et al., (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. et al., (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. et al., (1988) *Bio-Technology* 6:1197), or other nucleic acid amplification methods, followed by the detection of the amplified molecules using techniques known to those of skill in the art.

[00238] In another embodiment, mutations in an 84569 gene from a sample cell can be identified by detecting alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more

restriction endonucleases, and fragment length sizes are determined, e.g., by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

[00239] In other embodiments, genetic mutations in 84569 can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, two-dimensional arrays, e.g., chip based arrays. Such arrays include a plurality of addresses, each of which is positionally distinguishable from the other. A different probe is located at each address of the plurality. The arrays can have a high density of addresses, e.g., can contain hundreds or thousands of oligonucleotides probes (Cronin, M.T. et al., (1996) *Human Mutation* 7: 244-255; Kozal, M.J. et al., (1996) *Nature Medicine* 2:753-759). For example, genetic mutations in 84569 can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, M.T. et al., *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

[00240] In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the 84569 gene and detect mutations by comparing the sequence of the sample 84569 with the corresponding wild-type (control) sequence. Automated sequencing procedures can be utilized when performing the diagnostic assays ((1995) *Biotechniques* 19:448), including sequencing by mass spectrometry.

[00241] Other methods for detecting mutations in the 84569 gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers et al., (1985) *Science* 230:1242; Cotton et al., (1988) *Proc. Natl. Acad. Sci. USA* 85:4397; Saleeba et al., (1992) *Methods Enzymol.* 217:286-295).

[00242] In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point

mutations in 84569 cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu et al., (1994) *Carcinogenesis* 15:1657-1662; U.S. Patent No. 5,459,039).

[00243] In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in 84569 genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al., (1989) *Proc. Natl. Acad. Sci. USA*: 86:2766, see also Cotton, (1993) *Mutat. Res.* 285:125-144; and Hayashi, (1992) *Genet. Anal. Tech. Appl.* 9:73-79). Single-stranded DNA fragments of sample and control 84569 nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al., (1991) *Trends Genet.* 7:5).

[00244] In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al., (1985) *Nature* 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner, (1987) *Biophys. Chem.* 265:12753).

[00245] Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension (Saiki et al., (1986) *Nature* 324:163); Saiki et al., (1989) *Proc. Natl. Acad. Sci. USA* 86:6230).

[00246] Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of

interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al., (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner, (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al., (1992) *Mol. Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany, (1991) *Proc. Natl. Acad. Sci USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

[00247] The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an 84569 gene.

Use of 84569 Molecules as Surrogate Markers

[00248] The 84569 molecules of the invention are also useful as markers of disorders or disease states, as markers for precursors of disease states, as markers for predisposition of disease states, as markers of drug activity, or as markers of the pharmacogenomic profile of a subject. Using the methods described herein, the presence, absence and/or quantity of the 84569 molecules of the invention may be detected, and may be correlated with one or more biological states *in vivo*. For example, the 84569 molecules of the invention may serve as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is

desired before a potentially dangerous clinical endpoint is reached (e.g., an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

[00249] The 84569 molecules of the invention are also useful as pharmacodynamic markers. As used herein, a “pharmacodynamic marker” is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker (e.g., an 84569 marker) transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, anti-84569 antibodies may be employed in an immune-based detection system for an 84569 protein marker, or 84569-specific radiolabeled probes may be used to detect an 84569 mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

[00250] The 84569 molecules of the invention are also useful as pharmacogenomic markers. As used herein, a "pharmacogenomic marker" is an objective biochemical marker which correlates with a specific clinical drug response or susceptibility in a subject (see, e.g., McLeod *et al.* (1999) *Eur. J. Cancer* 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker is related to the predicted response of the subject to a specific drug or class of drugs prior to administration of the drug. By assessing the presence or quantity of one or more pharmacogenomic markers in a subject, a drug therapy which is most appropriate for the subject, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA, or protein (e.g., 84569 protein or RNA) for specific tumor markers in a subject, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be present in the subject. Similarly, the presence or absence of a specific sequence mutation in 84569 DNA may correlate 84569 drug response. The use of pharmacogenomic markers therefore permits the application of the most appropriate treatment for each subject without having to administer the therapy.

Pharmaceutical Compositions

[00251] The nucleic acid and polypeptides, fragments thereof, as well as anti-84569 antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical compositions. Such compositions typically include the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" includes solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Supplementary active compounds can also be incorporated into the compositions.

[00252] A pharmaceutical composition is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating

agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[00253] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[00254] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[00255] Oral compositions generally include an inert diluent or an edible carrier. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules, e.g., gelatin capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash.

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

[00256] For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

[00257] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

[00258] The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

[00259] In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to

viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

[00260] It is advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[00261] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit high therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[00262] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[00263] As defined herein, a therapeutically effective amount of protein or polypeptide (*i.e.*, an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, preferably about 0.01 to 25 mg/kg body weight, more preferably about 0.1 to 20 mg/kg body weight, and even more preferably about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight. The protein or polypeptide can be administered one time per

week for between about 1 to 10 weeks, preferably between 2 to 8 weeks, more preferably between about 3 to 7 weeks, and even more preferably for about 4, 5, or 6 weeks. The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments.

[00264] For antibodies, the preferred dosage is 0.1 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies.

Accordingly, lower dosages and less frequent administration is often possible.

Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (e.g., into the brain). A method for lipidation of antibodies is described by Cruikshank et al., ((1997) *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193).

[00265] The present invention encompasses agents which modulate expression or activity. An agent may, for example, be a small molecule. For example, such small molecules include, but are not limited to, peptides, peptidomimetics (e.g., peptoids), amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides, nucleotide analogs, organic or inorganic compounds (i.e., including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 500 grams per mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

[00266] Exemplary doses include milligram or microgram amounts of the small molecule per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram. It is furthermore understood that appropriate doses of a small molecule depend upon the potency of the small molecule with respect to the expression or activity to be modulated. When one

or more of these small molecules is to be administered to an animal (e.g., a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

[00267] An antibody (or fragment thereof) may be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

[00268] The conjugates of the invention can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte

macrophase colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

[00269] Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

[00270] The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (see U.S. Patent 5,328,470) or by stereotactic injection (see e.g., Chen et al., (1994) *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

[00271] The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Methods of Treatment:

[00272] The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant or unwanted 84569 expression or activity. With regards to both prophylactic and therapeutic methods of treatment, such treatments may be specifically tailored or modified, based on knowledge obtained from the field of pharmacogenomics. "Pharmacogenomics", as used herein, refers to the application of genomics technologies such as gene sequencing, statistical genetics, and gene expression analysis to drugs in clinical development and on the market. More specifically, the term refers the study of how a patient's genes determine his or her response to a drug (e.g., a patient's "drug response phenotype", or "drug response genotype".) Thus, another aspect of the invention provides methods for tailoring an individual's prophylactic or therapeutic treatment with either the 84569 molecules of the present invention or 84569 modulators according to that individual's drug response genotype. Pharmacogenomics allows a clinician or physician to target prophylactic or therapeutic treatments to patients who will most benefit from the treatment and to avoid treatment of patients who will experience toxic drug-related side effects.

[00273] In one aspect, the invention provides a method for preventing in a subject, a disease or condition associated with an aberrant or unwanted 84569 expression or activity, by administering to the subject an 84569 or an agent which modulates 84569 expression or at least one 84569 activity. Subjects at risk for a disease which is caused or contributed to by aberrant or unwanted 84569 expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the 84569 aberrance, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of 84569 aberrance, for example, an 84569 agonist or 84569 antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

[00274] It is possible that some 84569 disorders can be caused, at least in part, by an abnormal level of gene product, or by the presence of a gene product exhibiting abnormal activity. As such, the reduction in the level and/or activity of such gene products would bring about the amelioration of disorder symptoms.

[00275] As discussed, successful treatment of 84569 disorders can be brought about by techniques that serve to inhibit the expression or activity of target gene products. For example, compounds, e.g., an agent identified using an assays described above, that proves to exhibit negative modulatory activity, can be used in accordance with the invention to prevent and/or ameliorate symptoms of 84569 disorders. Such molecules can include, but are not limited to peptides, phosphopeptides, small organic or inorganic molecules, or antibodies (including, for example, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab')₂ and FAb expression library fragments, scFV molecules, and epitope-binding fragments thereof).

[00276] Further, antisense and ribozyme molecules that inhibit expression of the target gene can also be used in accordance with the invention to reduce the level of target gene expression, thus effectively reducing the level of target gene activity. Still further, triple helix molecules can be utilized in reducing the level of target gene activity. Antisense, ribozyme and triple helix molecules are discussed above.

[00277] It is possible that the use of antisense, ribozyme, and/or triple helix molecules to reduce or inhibit mutant gene expression can also reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by normal target gene alleles, such that the concentration of normal target gene product present can be lower than

is necessary for a normal phenotype. In such cases, nucleic acid molecules that encode and express target gene polypeptides exhibiting normal target gene activity can be introduced into cells via gene therapy method. Alternatively, in instances in that the target gene encodes an extracellular protein, it can be preferable to co-administer normal target gene protein into the cell or tissue in order to maintain the requisite level of cellular or tissue target gene activity.

[00278] Another method by which nucleic acid molecules may be utilized in treating or preventing a disease characterized by 84569 expression is through the use of aptamer molecules specific for 84569 protein. Aptamers are nucleic acid molecules having a tertiary structure which permits them to specifically bind to protein ligands (see, e.g., Osborne, et al., *Curr. Opin. Chem. Biol.* 1997, 1(1): 5-9; and Patel, D.J., *Curr. Opin. Chem. Biol.* 1997 Jun;1(1):32-46). Since nucleic acid molecules may in many cases be more conveniently introduced into target cells than therapeutic protein molecules may be, aptamers offer a method by which 84569 protein activity may be specifically decreased without the introduction of drugs or other molecules which may have pluripotent effects.

[00279] Antibodies can be generated that are both specific for target gene product and that reduce target gene product activity. Such antibodies may, therefore, be administered in instances whereby negative modulatory techniques are appropriate for the treatment of 84569 disorders. For a description of antibodies, see the Antibody section above.

[00280] In circumstances wherein injection of an animal or a human subject with an 84569 protein or epitope for stimulating antibody production is harmful to the subject, it is possible to generate an immune response against 84569 through the use of anti-idiotypic antibodies (see, for example, Herlyn, D., *Ann. Med.* 1999;31(1):66-78; and Bhattacharya-Chatterjee, M., and Foon, K.A., *Cancer Treat. Res.* 1998;94:51-68). If an anti-idiotypic antibody is introduced into a mammal or human subject, it should stimulate the production of anti-anti-idiotypic antibodies, which should be specific to the 84569 protein. Vaccines directed to a disease characterized by 84569 expression may also be generated in this fashion.

[00281] In instances where the target antigen is intracellular and whole antibodies are used, internalizing antibodies may be preferred. Lipofectin or liposomes can be used to deliver the antibody or a fragment of the Fab region that binds to the target antigen into cells. Where fragments of the antibody are used, the smallest inhibitory fragment that binds to the target antigen is preferred. For example, peptides having an amino acid sequence

corresponding to the Fv region of the antibody can be used. Alternatively, single chain neutralizing antibodies that bind to intracellular target antigens can also be administered. Such single chain antibodies can be administered, for example, by expressing nucleotide sequences encoding single-chain antibodies within the target cell population (see e.g., Marasco et al., (1993, *Proc. Natl. Acad. Sci. USA* 90:7889-7893).

[00282] The identified compounds that inhibit target gene expression, synthesis and/or activity can be administered to a patient at therapeutically effective doses to prevent, treat or ameliorate 84569 disorders. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of the disorders.

[00283] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds that exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[00284] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (i.e., the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

[00285] Another example of determination of effective dose for an individual is the ability to directly assay levels of “free” and “bound” compound in the serum of the test subject. Such assays may utilize antibody mimics and/or “biosensors” that have been created through molecular imprinting techniques. The compound which is able to modulate 84569

activity is used as a template, or “imprinting molecule”, to spatially organize polymerizable monomers prior to their polymerization with catalytic reagents. The subsequent removal of the imprinted molecule leaves a polymer matrix which contains a repeated “negative image” of the compound and is able to selectively rebind the molecule under biological assay conditions. A detailed review of this technique can be seen in Ansell, R. J. et al., (1996) *Current Opinion in Biotechnology* 7:89-94 and in Shea, K.J., (1994) *Trends in Polymer Science* 2:166-173. Such “imprinted” affinity matrixes are amenable to ligand-binding assays, whereby the immobilized monoclonal antibody component is replaced by an appropriately imprinted matrix. An example of the use of such matrixes in this way can be seen in Vlatakis, G. et al., (1993) *Nature* 361:645-647. Through the use of isotope-labeling, the “free” concentration of compound which modulates the expression or activity of 84569 can be readily monitored and used in calculations of IC₅₀.

[00286] Such “imprinted” affinity matrixes can also be designed to include fluorescent groups whose photon-emitting properties measurably change upon local and selective binding of target compound. These changes can be readily assayed in real time using appropriate fiberoptic devices, in turn allowing the dose in a test subject to be quickly optimized based on its individual IC₅₀. A rudimentary example of such a “biosensor” is discussed in Kriz, D. et al., (1995) *Analytical Chemistry* 67:2142-2144.

[00287] Another aspect of the invention pertains to methods of modulating 84569 expression or activity for therapeutic purposes. Accordingly, in an exemplary embodiment, the modulatory method of the invention involves contacting a cell with an 84569 or agent that modulates one or more of the activities of 84569 protein activity associated with the cell. An agent that modulates 84569 protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring target molecule of an 84569 protein (e.g., an 84569 substrate or ligand), an 84569 antibody, an 84569 agonist or antagonist, a peptidomimetic of an 84569 agonist or antagonist, or other small molecule.

[00288] In one embodiment, the agent stimulates one or 84569 activities. Examples of such stimulatory agents include active 84569 protein and a nucleic acid molecule encoding 84569. In another embodiment, the agent inhibits one or more 84569 activities. Examples of such inhibitory agents include antisense 84569 nucleic acid molecules, anti-84569 antibodies, and 84569 inhibitors. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the present invention provides methods of treating an

individual afflicted with a disease or disorder characterized by aberrant or unwanted expression or activity of an 84569 protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., upregulates or downregulates) 84569 expression or activity. In another embodiment, the method involves administering an 84569 protein or nucleic acid molecule as therapy to compensate for reduced, aberrant, or unwanted 84569 expression or activity.

[00289] Stimulation of 84569 activity is desirable in situations in which 84569 is abnormally downregulated and/or in which increased 84569 activity is likely to have a beneficial effect. For example, stimulation of 84569 activity is desirable in situations in which an 84569 is downregulated and/or in which increased 84569 activity is likely to have a beneficial effect. Likewise, inhibition of 84569 activity is desirable in situations in which 84569 is abnormally upregulated and/or in which decreased 84569 activity is likely to have a beneficial effect.

[00290] The 84569 molecules can act as novel diagnostic targets and therapeutic agents for controlling one or more of cellular proliferative and/or differentiative disorders, metabolic disorders, as described above. Diseases of metabolic imbalance include, but are not limited to, obesity, anorexia nervosa, cachexia, lipid disorders including hyperlipidemia, and diabetes.

Pharmacogenomics

[00291] The 84569 molecules of the present invention, as well as agents, or modulators which have a stimulatory or inhibitory effect on 84569 activity (e.g., 84569 gene expression) as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) 84569 associated disorders (e.g., cellular growth related disorders) associated with aberrant or unwanted 84569 activity. In conjunction with such treatment, pharmacogenomics (i.e., the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, a physician or clinician may consider applying knowledge obtained in relevant pharmacogenomics studies in determining whether to

administer an 84569 molecule or 84569 modulator as well as tailoring the dosage and/or therapeutic regimen of treatment with an 84569 molecule or 84569 modulator.

[00292] Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, for example, Eichelbaum, M. et al. (1996) *Clin. Exp. Pharmacol. Physiol.* 23(10-11):983-985 and Linder, M.W. et al. (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare genetic defects or as naturally-occurring polymorphisms. For example, glucose-6-phosphate dehydrogenase deficiency (G6PD) is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

[00293] One pharmacogenomics approach to identifying genes that predict drug response, known as "a genome-wide association", relies primarily on a high-resolution map of the human genome consisting of already known gene-related markers (e.g., a "bi-allelic" gene marker map which consists of 60,000-100,000 polymorphic or variable sites on the human genome, each of which has two variants.) Such a high-resolution genetic map can be compared to a map of the genome of each of a statistically significant number of patients taking part in a Phase II/III drug trial to identify markers associated with a particular observed drug response or side effect. Alternatively, such a high-resolution map can be generated from a combination of some ten million known single nucleotide polymorphisms (SNPs) in the human genome. As used herein, a "SNP" is a common alteration that occurs in a single nucleotide base in a stretch of DNA. For example, a SNP may occur once per every 1000 bases of DNA. A SNP may be involved in a disease process, however, the vast majority may not be disease-associated. Given a genetic map based on the occurrence of such SNPs, individuals can be grouped into genetic categories depending on a particular pattern of SNPs in their individual genome. In such a manner, treatment regimens can be tailored to groups of genetically similar individuals, taking into account traits that may be common among such genetically similar individuals.

[00294] Alternatively, a method termed the "candidate gene approach", can be utilized to identify genes that predict drug response. According to this method, if a gene that encodes a

drug's target is known (e.g., an 84569 protein of the present invention), all common variants of that gene can be fairly easily identified in the population and it can be determined if having one version of the gene versus another is associated with a particular drug response.

[00295] Alternatively, a method termed the "gene expression profiling", can be utilized to identify genes that predict drug response. For example, the gene expression of an animal dosed with a drug (e.g., an 84569 molecule or 84569 modulator of the present invention) can give an indication whether gene pathways related to toxicity have been turned on.

[00296] Information generated from more than one of the above pharmacogenomics approaches can be used to determine appropriate dosage and treatment regimens for prophylactic or therapeutic treatment of an individual. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an 84569 molecule or 84569 modulator, such as a modulator identified by one of the exemplary screening assays described herein.

[00297] The present invention further provides methods for identifying new agents, or combinations, that are based on identifying agents that modulate the activity of one or more of the gene products encoded by one or more of the 84569 genes of the present invention, wherein these products may be associated with resistance of the cells to a therapeutic agent. Specifically, the activity of the proteins encoded by the 84569 genes of the present invention can be used as a basis for identifying agents for overcoming agent resistance. By blocking the activity of one or more of the resistance proteins, target cells, e.g., cancer cells, will become sensitive to treatment with an agent that the unmodified target cells were resistant to.

[00298] Monitoring the influence of agents (e.g., drugs) on the expression or activity of an 84569 protein can be applied in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase 84569 gene expression, protein levels, or upregulate 84569 activity, can be monitored in clinical trials of subjects exhibiting decreased 84569 gene expression, protein levels, or downregulated 84569 activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease 84569 gene expression, protein levels, or downregulate 84569 activity, can be monitored in clinical trials of subjects exhibiting increased 84569 gene expression, protein levels, or upregulated 84569 activity. In such clinical trials, the expression or activity of an 84569 gene, and preferably, other genes that have been implicated in, for example, an

84569-associated disorder can be used as a "read out" or markers of the phenotype of a particular cell.

Other Embodiments

[00299] In another aspect, the invention features, a method of analyzing a plurality of capture probes. The method can be used, e.g., to analyze gene expression. The method includes: providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address of the plurality, and each address of the plurality having a unique capture probe, e.g., a nucleic acid or peptide sequence; contacting the array with an 84569, preferably purified, nucleic acid, preferably purified, polypeptide, preferably purified, or antibody, and thereby evaluating the plurality of capture probes. Binding, e.g., in the case of a nucleic acid, hybridization with a capture probe at an address of the plurality, is detected, e.g., by signal generated from a label attached to the 84569 nucleic acid, polypeptide, or antibody.

[00300] The capture probes can be a set of nucleic acids from a selected sample, e.g., a sample of nucleic acids derived from a control or non-stimulated tissue or cell.

[00301] The method can include contacting the 84569 nucleic acid, polypeptide, or antibody with a first array having a plurality of capture probes and a second array having a different plurality of capture probes. The results of each hybridization can be compared, e.g., to analyze differences in expression between a first and second sample. The first plurality of capture probes can be from a control sample, e.g., a wild type, normal, or non-diseased, non-stimulated, sample, e.g., a biological fluid, tissue, or cell sample. The second plurality of capture probes can be from an experimental sample, e.g., a mutant type, at risk, disease-state or disorder-state, or stimulated, sample, e.g., a biological fluid, tissue, or cell sample.

[00302] The plurality of capture probes can be a plurality of nucleic acid probes each of which specifically hybridizes, with an allele of 84569. Such methods can be used to diagnose a subject, e.g., to evaluate risk for a disease or disorder, to evaluate suitability of a selected treatment for a subject, to evaluate whether a subject has a disease or disorder. 84569 is associated with protein kinase activity, thus it is useful for disorders associated with abnormal lipid metabolism.

[00303] The method can be used to detect SNPs, as described above.

[00304] In another aspect, the invention features, a method of analyzing a plurality of probes. The method is useful, e.g., for analyzing gene expression. The method includes: providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address of the plurality having a unique capture probe, e.g., wherein the capture probes are from a cell or subject which express or mis express 84569 or from a cell or subject in which an 84569 mediated response has been elicited, e.g., by contact of the cell with 84569 nucleic acid or protein, or administration to the cell or subject 84569 nucleic acid or protein; contacting the array with one or more inquiry probe, wherein an inquiry probe can be a nucleic acid, polypeptide, or antibody (which is preferably other than 84569 nucleic acid, polypeptide, or antibody); providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address of the plurality, and each address of the plurality having a unique capture probe, e.g., wherein the capture probes are from a cell or subject which does not express 84569 (or does not express as highly as in the case of the 84569 positive plurality of capture probes) or from a cell or subject which in which an 84569 mediated response has not been elicited (or has been elicited to a lesser extent than in the first sample); contacting the array with one or more inquiry probes (which is preferably other than an 84569 nucleic acid, polypeptide, or antibody), and thereby evaluating the plurality of capture probes. Binding, e.g., in the case of a nucleic acid, hybridization with a capture probe at an address of the plurality, is detected, e.g., by signal generated from a label attached to the nucleic acid, polypeptide, or antibody.

[00305] In another aspect, the invention features, a method of analyzing 84569, e.g., analyzing structure, function, or relatedness to other nucleic acid or amino acid sequences. The method includes: providing an 84569 nucleic acid or amino acid sequence; comparing the 84569 sequence with one or more preferably a plurality of sequences from a collection of sequences, e.g., a nucleic acid or protein sequence database; to thereby analyze 84569.

[00306] Preferred databases include GenBank™. The method can include evaluating the sequence identity between an 84569 sequence and a database sequence. The method can be performed by accessing the database at a second site, e.g., over the internet.

[00307] In another aspect, the invention features, a set of oligonucleotides, useful, e.g., for identifying SNP's, or identifying specific alleles of 84569. The set includes a plurality of oligonucleotides, each of which has a different nucleotide at an interrogation position, e.g., an SNP or the site of a mutation. In a preferred embodiment, the oligonucleotides of

the plurality identical in sequence with one another (except for differences in length). The oligonucleotides can be provided with different labels, such that an oligonucleotides which hybridizes to one allele provides a signal that is distinguishable from an oligonucleotides which hybridizes to a second allele.

[00308] This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application, as well as in the Sequence Listing are incorporated herein by reference.

EXAMPLES

EXAMPLE 1: Identification and Characterization of Human 84569 cDNAs

[00309] The human 84569 sequence (SEQ ID NO:1), which is approximately 2230 nucleotides long including untranslated regions, contains a predicted methionine-initiated coding sequence of about 2208 nucleotides (nucleotides 1-2208 of SEQ ID NO:1; SEQ ID NO:3). The coding sequence encodes a 735 amino acid protein (SEQ ID NO:2).

EXAMPLE 2: 84569 Expression in Human and Mouse Tissues

[00310] Human RNA was purchased from Zen-Bio (adipose tissue and adipocyte samples), Clontech, or was prepared from samples available at Millennium. Tissues were collected from 10 week old male C57/B16J mice purchased from Zen-Bio, Inc. (Research Triangle Park, NC) or Clontech (Palo Alto, CA), or was prepared from other available tissue samples. Total RNA was prepared using the trizol method and treated with DNase to remove contaminating genomic DNA. cDNA was synthesized using standard techniques. Mock cDNA synthesis in the absence of reverse transcriptase resulted in samples with no detectable PCR amplification of the control 18S gene, confirming efficient removal of genomic DNA contamination. 84569 expression was measured by TaqMan quantitative PCR analysis, performed according to the manufacturer's directions (Perkin Elmer Applied Biosystems, Foster City, CA).

[00311] Normal human tissue samples included the following normal human tissues: aorta, veins, HUVEC, heart, kidney, skeletal muscle, liver, small intestine, adipose, pancreas, primary osteoblast, bladder, adrenal gland, pituitary gland, spinal cord, brain (cortex), brain (hypothalamus), nerve cells, dorsal root ganglion (DRG), breast, ovary, prostate, colon, lung, synovium, tonsil, lymph node, spleen, macrophages, thymus,

megakaryocytes, progenitor cells, neutrophils, erythroid, and activated PBMC. Additionally tested were selected diseases tissues (see Table 2).

[00312] Normal mouse tissues examined included the following: heart, brown fat, lung, liver, kidney, skeletal muscle, diaphysis, metaphysis, pancreas, spleen, testis, calvaria brain/hypothalamus, and hypothalamus.

[00313] PCR probes were designed by PrimerExpress software (PE Biosystems) based on the respective sequences of murine and human 84569. To standardize the results between the different tissues, two probes, distinguished by different fluorescent labels, were added to each sample. The differential labeling of the probe for the 84569 and the probe for 18S RNA (as an internal control) thus enabled their simultaneous measurement in the same well. Forward and reverse primers and the probes for both 18S RNA and human or murine 84569 were added to the TaqMan Universal PCR Master Mix (PE Applied Biosystems). Although the final concentration of primer and probe could vary, each was internally consistent within a given experiment. A typical experiment contained 200 nM each of the forward and reverse primers and 100 nM of the probe for the 18S RNA, as well as 600 nM of each of the forward and reverse primers and 200 nM of the probe for 84569. TaqMan matrix experiments were carried out using an ABI PRISM 770 Sequence Detection System (PE Applied Biosystems). The thermal cycler conditions were as follows: hold for 2 minutes at 50 °C and 10 minutes at 95 °C, followed by two-step PCR for 40 cycles of 95 °C for 15 seconds, followed by 60 °C for 1 minute.

[00314] The following method was used to quantitatively calculate 84569 gene expression in the tissue samples, relative to the 18S RNA expression in the same tissue. The threshold values at which the PCR amplification started were determined using the manufacturer's software. PCR cycle number at threshold value was designated as CT. Relative expression was calculated as $2^{-((CT_{\text{test}} - CT_{18S})_{\text{tissue of interest}} - (CT_{\text{test}} - CT_{18S})_{\text{lowest expressing tissue in panel}})}$. Samples were run in duplicate and the averages of 2 relative expression levels that were linear to the amount of template cDNA with a slope similar to the slope for the internal control 18S were used.

[00315] The results of expression of 84569 in human tissues by TaqMan analysis showed significant levels of expression of 84569 in brain hypothalamus, with lower levels of expression detected in ovary, and lung tissues. Furthermore, 84569 was present in brain hypothalamic tissue at considerably higher levels compared to brain cortex (see e.g., Table

2). These data indicate that 84569 is preferentially expressed in tissues relevant to regulation of metabolic disease (e.g., hypothalamus).

TABLE 2 84569 Expression in Human Multi-Tissue Panel

Tissue Type	Expression	Tissue Type	Expression
Artery normal	0.0079259	Breast normal	0.0074724
Aorta diseased	0.0405483	Breast Tumor	0.0038949
Vein normal	0.0073695	Ovary normal	2.122529
Coronary SMC	0.0037752	Ovary Tumor	0.1529131
HUVEC	0.0084653	Prostate BPH	0.0054512
Hemangioma	0.003672	Prostate Tumor	0.0411143
Heart normal	0.0037492	Colon normal	0.0031418
Heart CHF	0.0116849	Colon Tumor	0.0065051
Kidney	0.0074983	Lung normal	0.1482171
Skeletal Muscle	0.1059007	Lung tumor	5.3176333
Liver normal	0.005585	Lung COPD	3.5696541
Small intestine	0.0076294	Colon IBD	0.0079534
Adipose normal	0.0038949	Synovium	0.0035347
Pancreas	0.0220326	Tonsil normal	0.0019474
primary osteoblast	0.0041889	Lymph node normal	0.0058831
Bladder	0.0030242	Liver fibrosis	0.0087639
Adrenal Gland	0.0032638	Spleen normal	0.0013487
Pituitary Gland	0.0132376	Macrophages	0.0004988
Spinal cord	0.1513315	Progenitors (erythroid, megakaryocyte, neutrophil)	0.0040743
Brain Cortex normal	0.0191805	Megakaryocytes	0.0031309
Brain Hypothalamus normal	37.812315	Activated PBMC	0.0011539
Nerve	0.008177	Neutrophils	0.0025168
NTC	1000	Erythroid	0.0125235
DRG (Dorsal Root Ganglion)	0.0138957	positive control	179.24441

[00316] TaqMan analysis was also performed in mouse tissues as indicated above. Consistent with the human results, 84569 was highly expressed in brain and hypothalamus tissue, but was present at considerably lower levels in most other tissues tested (see e.g., Table 2). Some expression was seen in spleen and lung.

TABLE 3 84569 Expression in Mouse Multi-tissue Panel

Tissue Type	Expression
heart	0.00
brown fat	0.00
lung	6.70
liver	0.00
kidney	0.00
sk muscle	0.00
diaphysis	0.00
metaphysis	0.00
pancreas	0.00
spleen	4.89
testis	0.00
calvaria	0.00
brain2	0.00
hypo2	32.70

EXAMPLE 2: Localization of 84569 Expression

[00317] To further confirm the TaqMan expression data, additional Taqman analysis on tissues isolated from regions of mouse hypothalamus was assessed, as well as *In situ* hybridization analysis of mouse brain tissues performed using a probe of the mouse 84569 gene. Coronal sections from mouse brain 280 mm in thickness that span 3 mm caudal to the paraventricular nucleus and rostral to the arcuate nucleus (all within the hypothalamic region) were generated and stored at -80 C. Micro-dissection to isolate the body weight nuclei including the arcuate, paraventricular, dorsal medial, ventral medial areas as well as the lateral hypothalamic region were performed using Palvovitz micro-dissection needles (Stoelting Co.; Cat # 57401) for use in standard RNA extraction procedures and Taqman analysis as described above. Table 4 depicts relative expression level results indicating 84569 expression is highest in arcuate and ventromedial nuclei regions of the hypothalamus, and this expression is significantly higher than whole hypothalamus samples. These data are in agreement with the TaqMan panel expression data and demonstrate that the brain, particularly the hypothalamus, is a major site of 84569 expression.

TABLE 4 Enriched 84569 Expression in ARC/VMH

Sample	Expression
Ctrl ARC/VMH	45.1
Ctrl hypo	5.4

[00318] 84569 expression in normal mouse brain tissue was also measured by *in situ* hybridization analysis. For *in situ* analysis, various tissues, *e.g.* tissues obtained from brain, were first frozen on dry ice. Ten-micrometer-thick sections of the tissues were post-fixed with 4% formaldehyde in DEPC treated 1X phosphate- buffered saline at room temperature for 10 minutes before being rinsed twice in DEPC 1X phosphate-buffered saline and once in 0.1 M triethanolamine-HCl (pH 8.0). Following incubation in 0.25% acetic anhydride-0.1 M triethanolamine-HCl for 10 minutes, sections were rinsed in DEPC 2X SSC (1X SSC is 0.15M NaCl plus 0.015M sodium citrate). Tissue was then dehydrated through a series of ethanol washes, incubated in 100% chloroform for 5 minutes, and then rinsed in 100% ethanol for 1 minute and 95% ethanol for 1 minute and allowed to air dry.

[00319] 84569 expression in normal mouse brain tissue was also measured by *in situ* hybridization analysis. For *in situ* analysis, various tissues, *e.g.* tissues obtained from brain, were first frozen on dry ice. Ten-micrometer-thick sections of the tissues were post-fixed with 4% formaldehyde in DEPC treated 1X phosphate- buffered saline at room temperature for 10 minutes before being rinsed twice in DEPC 1X phosphate-buffered saline and once in 0.1 M triethanolamine-HCl (pH 8.0). Following incubation in 0.25% acetic anhydride-0.1 M triethanolamine-HCl for 10 minutes, sections were rinsed in DEPC 2X SSC (1X SSC is 0.15M NaCl plus 0.015M sodium citrate). Tissue was then dehydrated through a series of ethanol washes, incubated in 100% chloroform for 5 minutes, and then rinsed in 100% ethanol for 1 minute and 95% ethanol for 1 minute and allowed to air dry.

[00320] Hybridizations were performed with ³⁵S-radiolabeled (5×10^7 cpm/ml) cRNA probes. Probes were incubated in the presence of a solution containing 600 mM NaCl, 10 mM Tris (pH 7.5), 1 mM EDTA, 0.01% sheared salmon sperm DNA, 0.01% yeast tRNA, 0.05% yeast total RNA type X1, 1X Denhardt's solution, 50% formamide, 10% dextran sulfate, 100 mM dithiothreitol, 0.1% sodium dodecyl sulfate (SDS), and 0.1% sodium thiosulfate for 18 hours at 55°C.

[00321] After hybridization, slides were washed with 2X SSC. Sections were then sequentially incubated at 37°C in TNE (a solution containing 10 mM Tris-HCl (pH 7.6), 500

mM NaCl, and 1 mM EDTA), for 10 minutes, in TNE with 10 µg of RNase A per ml for 30 minutes, and finally in TNE for 10 minutes. Slides were then rinsed with 2X SSC at room temperature, washed with 2X SSC at 50°C for 1 hour, washed with 0.2X SSC at 55°C for 1 hour, and 0.2X SSC at 60°C for 1 hour. Sections were then dehydrated rapidly through serial ethanol-0.3 M sodium acetate concentrations before being air dried and exposed to Kodak Biomax MR scientific imaging film for 24 hours and subsequently dipped in NB-2 photoemulsion and exposed at 4°C for 7 days before being developed and counter stained.

[00322] In situ hybridization analysis revealed that 84569 is expressed at a much higher level in the hypothalamus than in other areas of the brain. Further localization of 84569 expression in the hypothalamic region demonstrated through *in situ* analysis confirmed the expression was localized to the arcuate/VMH region of the hypothalamus and ependyma region of the ventricle/choroid plexus.

EXAMPLE 3: Regulation of 84569 in genetically obese mice

[00323] To determine whether 84569 is regulated in obese, insulin-resistant mice, we examined expression in genetically obese ob/ob mice and agouti Ag mice. 84569 expression was considerably higher in hypothalamus of ob/ob mice and Ag mice as compared to wild-type control mice (See Table 5).

[00324] Expression regulation of 84569 was also examined in response to fasting and/or leptin treatment, however, no response to short term fasting/refeeding or leptin treatment of animals was detected.

TABLE 5: Enriched 84569 Expression in Hypothalamus of Ag and ob/ob mice

Sample	Expression
Ag hypothalamus	2.57
OB hypothalamus	4.03
WT hypothalamus	1.00

EXAMPLE 4: Overexpression of 84569 Can Affect Leptin Receptor Signaling

[00325] To determine if expression of 84569 affected leptin signal transduction activity, GT1-7 cells were cotransfected using the lipofectamine method with OB-R_L(wt) and reporter gene constructs containing regulatory elements responsive to OB-R_L signals. Cells were also co-transfected with 84569 cDNA or with control vector. The methods and constructs have been described previously. See White, D.W., et al. (1997) *Proc. Natl. Acad. Sci. USA*

94, pp. 10657-10662. Cultures overexpressing 84569 exhibited diminished reporter gene activity as compared to strong ligand-dependent induction of reporter gene activity in control cultures (See Table 6).

TABLE 6: 84569 expression affects leptin receptor signaling

	<u>Leptin</u>	<u>Reporter Activity</u>
GT1-7 cells	-	3041
	+	27005
84569 expression	-	4146
	+	7604
Vector control	-	4316.5
	+	25023.5

Equivalents

[00325] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.